

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:08:34 ; Search time 811.38 Seconds
(without alignments)
618.773 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTCGTGACTTT 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	38.7	50	9	AU106272
2	12	38.7	50	9	AU106275
3	12	38.7	50	9	AU106276
4	12	38.7	50	9	AU106277
5	12	38.7	50	9	AU106279
6	12	38.7	50	9	AU106287

C	7	11	35.5	25	9	AI620546	tu95b04.x
C	8	11	35.5	26	17	AZ362697	1M0107G23
C	9	11	35.5	31	9	AI744856	tr16a11.x
C	10	11	35.5	39	9	AA757804	zg44a08.8
C	11	11	35.5	40	9	AI630923	tz31h05.x
C	12	11	35.5	49	9	AI253403	aq14c09.x
C	13	11	35.5	50	9	AU105311	AU105311
C	14	10	32.3	19	17	AZ612624	1M0439C04
C	15	10	32.3	20	17	AZ816496	2M0085G16
C	16	10	32.3	22	9	AI664440	ue62c03.r
C	17	10	32.3	27	17	AZ783540	2M0025G22
C	18	10	32.3	28	9	AI244530	qk14d06.x
C	19	10	32.3	29	9	AU014027	AU014027
C	20	10	32.3	30	10	BE297610	601178187
C	21	10	32.3	30	17	AZ598617	AZ598617
C	22	10	32.3	32	9	AU014022	AU014022
C	23	10	32.3	33	9	AU256484	AU256484
C	24	10	32.3	33	14	T73421	YC35a08.81
C	25	10	32.3	35	14	T73795	YC54a06.81
C	26	10	32.3	37	9	AI698327	tx63c12.x
C	27	10	32.3	37	9	AA588127	nk10h05.8
C	28	10	32.3	37	17	AZ472879	1M0288H24
C	29	10	32.3	38	17	AZ779310	2M0015M05
C	30	10	32.3	39	14	T70882	YC49a04.81
C	31	10	32.3	39	17	AZ824330	2M0098C22
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C	33	10	32.3	40	9	AI188838	qd21f12.x
C	34	10	32.3	40	9	AI684941	wa74d06.x
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C	36	10	32.3	45	14	T69149	YC32b08.81
C	37	10	32.3	45	14	T71655	YC62b05.81
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C	40	10	32.3	46	17	BH853626	BH853626
C	41	10	32.3	48	17	AZ464204	1M0273A03
C	42	10	32.3	49	9	AA130544	zol2f06.r
C	43	10	32.3	49	9	AI565007	tg53d09.x
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C	45	10	32.3	50	9	AU102670	AU102670

ALIGNMENTS

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LOCUS AU106272 50 bp mRNA linear EST 30-AUG-2001
DEFINITION HRC00538, mRNA sequence.
ACCESSION AU106272
VERSION AU106272.1 GI:13555793
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

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1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC00538"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 CCGCGCGCTGTT 16
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Db      23 CCGCGCGCTGTT 34

RESULT 2
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LOCUS      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION      Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION      AUI06275
VERSION      AUI06275
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
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dimethylfumarate treated U937 cells"
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 CCGCGCGCTGTT 16
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Db      32 CCGCGCGCTGTT 43

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LOCUS      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION      Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION      AUI06277
VERSION      AUI06277
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC02715"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 CCGCGCGCTGTT 16
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Db      23 CCGCGCGCTGTT 34

RESULT 3
AUI06276
LOCUS      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION      Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION      AUI06276
VERSION      AUI06276
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 50)
AUTHORS      Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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/note="Differential display comparison of untreated and
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
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Db. 20 CCGCGCGCTGTT 31

RESULT 5
AUI06279
LOCUS      50 bp mRNA linear EST 30-AUG-2001
DEFINITION HRC06165, mRNA sequence.
ACCESSION  AUI06279
VERSION     AUI06279
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 33 CCGCGCGCTGTT 44

RESULT 6
AUI06287
LOCUS      50 bp mRNA linear EST 30-AUG-2001
DEFINITION ADSU02137, mRNA sequence.
ACCESSION  AUI06287
VERSION     AUI06287
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 33 CCGCGCGCTGTT 44

RESULT 6
AUI06287
LOCUS      50 bp mRNA linear EST 30-AUG-2001
DEFINITION ADSU02137, mRNA sequence.
ACCESSION  AUI06287
VERSION     AUI06287
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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BASE COUNT      3 a      24 c      16 g      7 t
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Query Match      38.7%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
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Db. 33 CCGCGCGCTGTT 44

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LOCUS      25 bp mRNA linear EST 15-DEC-1999
DEFINITION tu95b04.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258767 3'
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ACCESSION  AUI06287/c
VERSION     AUI06287/c
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 25)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Sequencing by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
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Seq primer: -400P from Gibco
High quality sequence stop: 1
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SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Query Match      38.7%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGCGCGCTGTT 16
    |||||
Db. 33 CCGCGCGCTGTT 44

RESULT 7
AUI06287/c
LOCUS      25 bp mRNA linear EST 15-DEC-1999
DEFINITION tu95b04.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258767 3'
            similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ; , mRNA sequence.
ACCESSION  AUI06287/c
VERSION     AUI06287/c
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 25)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Sequencing by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1315 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1
POLYA=No.

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FEATURES
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        /lab_host="DH10B"
        /note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
        Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 1.69 kb. Life Technologies catalog #:
        11549-011"
BASE COUNT      16 a      7 c      2 g      0 t
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Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GCTGTTTCTTCT 21
        |||||
Db       22 GCTGTTTCTTCT 12

RESULT 8
AZ362697/c
LOCUS      AZ362697      26 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION      1M0107G23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                  clone UUGCIM0107G23 R, DNA sequence.
ACCESSION      AZ362697
VERSION      AZ362697.1 GI:10476397
KEYWORDS      GSS.
SOURCE      house mouse
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 26)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: G column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
  1..26
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGCIM0107G23"
    /clone_lib="Mouse 10kb plasmid UUGCIM library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
  
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

BASE COUNT      1 a      3 c      19 g      3 t
ORIGIN

```

```

Query Match      35.5%; Score 11; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 CCCC GCCGCGCT 13
        |||||
Db       11 CCCC GCCGCGCT 1

```

```

RESULT 9
AI744856/c
LOCUS      AI744856      31 bp      mRNA      linear      EST 21-JUN-1999
DEFINITION      tr16a1.x1 NCI CGAP Ov23 Homo sapiens CDNA clone IMAGE:2218460 3,
                  similar to TR:Q33564 Q33564 EATRO 184 KINETOPLAST; contains element
                  TARI repetitive element; mRNA sequence.
ACCESSION      AI744856
VERSION      AI744856.1 GI:5113144
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 31)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

```

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
  1..31
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:2218460"
    /clone_lib="NCI CGAP_Ov23"
    /tissue_type="tumor, 5 pooled (see description)"
    /lab_host="DH10B"
    /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.35 kb. Tumor types include: mixed
    Mullerian tumor, papillary serous, clear cell, spindle
    cell. All are primary tumors, metastasis positive. Life
    Technologies catalog #: 11534-013"

```

```

FEATURES
  source
    Location/Qualifiers

```

```

BASE COUNT      19 a      3 c      7 g      2 t
ORIGIN

```

Query Match 35.5%; Score 11; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCGTTTTCCTC 22
 Db 16 CCGTTTTCCTC 6

RESULT 10
 AA757804/c
 LOCUS
 DEFINITION 39 bp mRNA linear EST 23-JAN-1998
 2944a08.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
 IMAGE:396182 3' similar to gb:223090 HEAT SHOCK 27 KD PROTEIN
 (HUMAN); mRNA sequence.

ACCESSION
 VERSION
 AA757804.1 GI:2805667
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 39)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
 , J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)

TITLE
 JOURNAL
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..39
 /organism="Homo sapiens"
 /db_xref="GDB:1302084"
 /db_xref="taxon:9606"
 /clone="IMAGE:396182"
 /clone_lib="Soares_pineal_gland_N3HPG"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 1st strand cDNA was primed with a Not I - oligo(dT) primer
 [5' TGTTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
 , double-stranded cDNA was size selected, ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

BASE COUNT 15 a 3 c 10 g 11 t

Query Match 35.5%; Score 11; DB 9; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCGTTTTCCTC 22
 Db 33 CCGTTTTCCTC 23

RESULT 11
 AI630923
 LOCUS

AI630923 40 bp mRNA linear EST 16-DEC-1999

DEFINITION t23lh05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2290233 3'
 similar to SW:SP49 HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTEIN 49
 ;contains TAR1.t3 MSRI repetitive element ;, mRNA sequence.

ACCESSION
 VERSION
 AI630923.1 GI:4682253
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 40)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)

JOURNAL
 COMMENT
 Email: cgapba-r@mail.nih.gov
 Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1907 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..40
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2290233"
 /clone_lib="NCI-CGAP Ut2"
 /tissue_type="moderately-differentiated endometrial
 adenocarcinoma, 3 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.85 kb. Life Technologies catalog #:
 11539-012"

BASE COUNT 2 a 26 c 8 g 4 t

Query Match 35.5%; Score 11; DB 9; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGCGCGGCT 13
 Db 4 CCGCGCGGCT 14

RESULT 12
 AI253403
 LOCUS

DEFINITION AI253403 49 bp mRNA linear EST 06-NOV-1998
 aq14c09.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone
 IMAGE:2030896 similar to FR:Q33559 Q33559 NH2 TERMINUS UNCERTAIN ;,
 mRNA sequence.

ACCESSION
 VERSION
 AI253403.1 GI:3850358
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 49)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
 , J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LILNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
source
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2030896"
/clone_lib="Stanley Frontal NS pool 2"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
before use) was reverse transcribed using a modified
oligo-dT primer containing Real and HindIII sites.
Double-stranded cDNA was digested with Real, resulting in
blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor
(5'-TCGAGCGCGCGCGGCGGT-3' or 5'-
AGGCGTGTGGCGGCGGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select
cDNA subtraction kit. Pool of two mentally normal male
individuals ages 41 and 53 (S-124, S-141) subtracted by
pool of two schizophrenic individuals, male age 44 and
female age 56 (S-116, S-118). Tissues were obtained from
the Stanley Neuropathology Consortium (www.stanleylab.org
). Library constructed and subtracted by Dr. Nancy
Johnston [(410) 614-3918, nj@weilink.uch.edu]."
BASE COUNT 5 a 11 c 6 g 27 t
ORIGIN
Query Match 35.5%; Score 11; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CTGTTTTC TC 22
Db 28 CTGTTTTC TC 38
RESULT 13
AUI05311/c
LOCUS AUI05311
DEFINITION AUI05311 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADKA01517, mRNA sequence.
ACCESSION AUI05311
VERSION AUI05311.1 GI:13554832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADKA01517"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 7 a 19 c 13 g 11 t
ORIGIN
Query Match 35.5%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CCGCGCGCTGT 15
Db 17 CCGCGCGCTGT 7
RESULT 14
AZ612624
LOCUS AZ612624
DEFINITION IM0439C04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0439C04 R, DNA sequence.
ACCESSION AZ612624
VERSION AZ612624.1 GI:11734730
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0439 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
source
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0439C04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 5 c 7 g 7 t
ORIGIN

Query Match 32.3%; Score 10; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCGCTGTTT 17
|||||
DB 4 CGCGCTGTTT 13

RESULT 15
AZ816496
LOCUS
DEFINITION 20 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0085G16 F, DNA sequence.
ACCESSION AZ816496
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Royagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0085 row: G column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0085G16"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 3 c 3 g 14 t
ORIGIN

Query Match 32.3%; Score 10; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTTTTTCT 21
|||||
DB 10 CTGTTTTTCT 19

Search completed: June 24, 2003, 16:52:48
Job time : 814.38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:09:29 ; Search time 1721.65 Seconds
(without alignments)
125.426 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTCGTCACTTT 31

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7821610 seqs, 3482903955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8654690

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents NA New.*
1: /cgn2_6/ptodata/2/pna/US06_PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*
12: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*
13: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	9	US-10-359-935-22
C 2	21	67.7	28	9	US-10-359-935-29
C 3	19	61.3	19	1	PCT-US03-04088-11
C 4	19	61.3	19	1	PCT-US03-04088-275
C 5	14	45.2	25	7	US-09-954-445A-120839
C 6	14	45.2	25	7	US-09-954-445A-120843
C 7	14	45.2	25	7	US-09-954-445A-120845
C 8	14	45.2	25	12	US-60-427-836-342410
C 9	13	41.9	25	7	US-09-954-445A-31235
C 10	13	41.9	25	7	US-09-954-445A-31237
C 11	13	41.9	25	7	US-09-954-445A-31253
C 12	13	41.9	25	9	US-10-294-038-3446
C 13	13	41.9	25	9	US-10-355-577-88370
C 14	13	41.9	25	9	US-10-355-577-738956
C 15	13	41.9	25	9	US-10-355-577-738956
C 16	13	41.9	25	9	US-10-355-577-973292
C 17	13	41.9	25	10	US-10-367-892-80
C 18	13	41.9	25	10	US-10-367-892-21888
C 19	13	41.9	25	10	US-10-294-038A-3446
C 20	13	41.9	25	12	US-60-427-808-20286

C 21	13	41.9	25	12	US-60-427-808-26051	Sequence 26051, A
C 22	13	41.9	25	12	US-60-427-808-66169	Sequence 66169, A
C 23	13	41.9	25	12	US-60-427-808-583626	Sequence 583626, A
C 24	13	41.9	25	12	US-60-427-836-4638	Sequence 4638, Ap
C 25	13	41.9	25	12	US-60-427-836-105088	Sequence 105088, A
C 26	13	41.9	40	9	US-10-294-038-686	Sequence 686, App
C 27	13	41.9	40	10	US-10-294-038A-686	Sequence 686, App
C 28	12	38.7	15	9	US-10-303-778-6395	Sequence 6395, Ap
C 29	12	38.7	15	9	US-10-310-188-44983	Sequence 44983, A
C 30	12	38.7	17	9	US-10-310-188-78585	Sequence 78585, A
C 31	12	38.7	17	9	US-10-310-188-84695	Sequence 84695, A
C 32	12	38.7	18	9	US-10-303-778-5689	Sequence 5689, Ap
C 33	12	38.7	18	9	US-10-310-188-78276	Sequence 78276, A
C 34	12	38.7	19	1	PCT-US03-04088-12	Sequence 12, Appl
C 35	12	38.7	19	1	PCT-US03-04088-276	Sequence 276, App
C 36	12	38.7	19	9	US-10-310-188-85526	Sequence 85526, A
C 37	12	38.7	19	10	US-10-367-892-79	Sequence 79, Appl
C 38	12	38.7	19	10	US-10-367-892-14893	Sequence 14893, A
C 39	12	38.7	19	10	US-10-367-892-22556	Sequence 22556, A
C 40	12	38.7	20	9	US-10-348-485-21	Sequence 21, Appl
C 41	12	38.7	20	9	US-10-348-485-22	Sequence 22, Appl
C 42	12	38.7	21	9	US-10-310-188-77351	Sequence 77351, A
C 43	12	38.7	22	9	US-10-310-188-40698	Sequence 40698, A
C 44	12	38.7	25	6	US-09-660-222-63498	Sequence 63498, A
C 45	12	38.7	25	7	US-09-954-445A-87073	Sequence 87073, A

ALIGNMENTS

RESULT 1
US-10-359-935-22/c
; Sequence 22, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villegonteau, Bryant
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-10-359-935-22

Query Match 71.0%; Score 22; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
 DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 2

US-10-359-935-29/c
 Sequence 29, Application US/10359935
 GENERAL INFORMATION:
 APPLICANT: Villeponteau, Bryant
 Funk, Junli
 Andrews, William H.
 TITLE OF INVENTION: Mammalian Telomerase
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/359,935
 FILING DATE: 07-Feb-2003
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/057,351
 FILING DATE: 08-APR-1994
 APPLICATION NUMBER: US 08/272,102
 FILING DATE: 07-JUL-1994
 APPLICATION NUMBER: US 08/330,123
 FILING DATE: 27-OCT-1994
 APPLICATION NUMBER: US 08/472,802
 FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 015389-000821US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-359-935-29

Query Match 67.7%; Score 21; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.065;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 21
 DB 21 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 3

PCT-US03-04088-11
 Sequence 11, Application PC/TUS0304088
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: McSwiggen, James
 APPLICANT: Beigelman, Leonid
 TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 FILE REFERENCE: 02-708-A (400/080)
 CURRENT APPLICATION NUMBER: PCT/US03/04088
 CURRENT FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: US 60/396,600
 PRIOR FILING DATE: 2002-07-17
 PRIOR APPLICATION NUMBER: US 60/358,580
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 60/363,124
 PRIOR FILING DATE: 2002-03-11
 PRIOR APPLICATION NUMBER: US 60/386,782
 PRIOR FILING DATE: 2002-06-06
 PRIOR APPLICATION NUMBER: US 60/406,784
 PRIOR FILING DATE: 2002-08-29
 PRIOR APPLICATION NUMBER: US 60/408,378
 PRIOR FILING DATE: 2002-09-05
 PRIOR APPLICATION NUMBER: US 60/409,293
 PRIOR FILING DATE: 2002-09-09
 PRIOR APPLICATION NUMBER: US 60/440,129
 PRIOR FILING DATE: 2003-01-15
 NUMBER OF SEQ ID NOS: 626
 SOFTWARE: Patent in version 3.2
 SEQ ID NO 11

LENGTH: 19
 TYPE: RNA
 ORGANISM: Artificial
 FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 OTHER INFORMATION: region
 PCT-US03-04088-11

Query Match 61.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 63.2%; Pred. No. 0.85; 0; Indels 0; Gaps 0;
 Matches 12; Conservative 7; Mismatches 0

QY 2 TCCCTCCGCGCGCTGTTTCTC 20
 DB 1 UCCCTCCGCGCGUGUUUUC 19

RESULT 4

PCT-US03-04088-275/c
 Sequence 275, Application PC/TUS0304088
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: McSwiggen, James
 APPLICANT: Beigelman, Leonid
 TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 FILE REFERENCE: 02-708-A (400/080)
 CURRENT APPLICATION NUMBER: PCT/US03/04088
 CURRENT FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: US 60/396,600
 PRIOR FILING DATE: 2002-07-17
 PRIOR APPLICATION NUMBER: US 60/358,580
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 60/363,124
 PRIOR FILING DATE: 2002-03-11
 PRIOR APPLICATION NUMBER: US 60/386,782

;
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-275

Query Match 61.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TCCCGCGCGCTGTTTTC 20
Db 19 TCCCGCGCGCTGTTTTC 1

RESULT 5
US-09-954-445A-120839
; Sequence 120839, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-120839

Query Match 45.2%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GCGCTGTTTTC 22
Db 1 GCGCTGTTTTC 14

RESULT 6
US-09-954-445A-120843
; Sequence 120843, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120843
; LENGTH: 25
; TYPE: DNA

;
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-120843

Query Match 45.2%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GCGCTGTTTTC 22
Db 9 GCGCTGTTTTC 22

RESULT 7
US-09-954-445A-120845
; Sequence 120845, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-120845

Query Match 45.2%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GCGCTGTTTTC 22
Db 6 GCGCTGTTTTC 19

RESULT 8
US-60-427-836-342410/C
; Sequence 342410, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 342410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-342410

Query Match 45.2%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 CTGTTTTCTCGCT 25
Db 15 CTGTTTTCTCGCT 2

RESULT 9
US-09-954-445A-31235
; Sequence 31235, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1

; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31235
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-31235

Query Match 41.9%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCTG 26
|||||
DB 6 GTTTTCTCGCTG 18

RESULT 10
US-09-954-445A-31237
; Sequence 31237, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31237
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-31237

Query Match 41.9%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCTG 26
|||||
DB 2 GTTTTCTCGCTG 14

RESULT 11
US-09-954-445A-31253
; Sequence 31253, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31253
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-31253

Query Match 41.9%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCTG 26

DB 12 GTTTTCTCGCTG 24
|||||

RESULT 12
US-10-294-038-3446/c
; Sequence 3446, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 3446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (1583792)...(1583815)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4331
US-10-294-038-3446

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTCTCGCTGAC 28
|||||
DB 18 TTTTCTCGCTGAC 6

RESULT 13
US-10-355-577-88370
; Sequence 88370, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-88370

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTTTCTCGCTG 25
|||||
DB 12 TTTTCTCGCTG 24

RESULT 14
US-10-355-577-724663
; Sequence 724663, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 724663
; LENGTH: 25
; TYPE: DNA

; ORGANISM: Homo sapien
US-10-355-577-724663

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTTCCTCGCT 25
|||
Db 4 TGTTCCTCGCT 16

RESULT 15

US-10-355-577-738956
; Sequence 738956, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 738956
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-738956

Query Match 41.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTTCCTCGCT 25
|||
Db 13 TGTTCCTCGCT 25

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Job time : 1721.65 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:01:44 ; Search time 1340.69 Seconds
(without alignments)
581.357 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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73: /cgn2_6/ptodata/2/pna/us6029 COMB.seq.*
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84: /cgn2_6/ptodata/2/pna/us6040 COMB.seq.*
85: /cgn2_6/ptodata/2/pna/us6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	22	71.0	30	7	US-08-387-524-18
C 3	22	71.0	30	8	US-08-472-802A-23
C 4	22	71.0	30	8	US-08-472-802B-23
C 5	22	71.0	30	8	US-08-482-115A-22
C 6	22	71.0	30	9	US-08-520-550-18
C 7	22	71.0	30	9	US-08-521-634-40
C 8	22	71.0	30	10	US-08-660-678-22
C 9	22	71.0	30	14	US-09-057-351-22
C 10	22	71.0	30	16	US-09-259-943-44
C 11	21	67.7	28	8	US-08-472-802A-29
C 12	21	67.7	28	8	US-08-472-802B-29
C 13	21	67.7	28	8	US-08-482-115A-28
C 14	21	67.7	28	9	US-08-521-634-47
C 15	21	67.7	28	14	US-09-057-351-29
C 16	21	67.7	30	7	US-08-387-524-34
C 17	21	67.7	30	9	US-08-520-550-34
C 18	21	67.7	30	16	US-09-259-943-60
C 19	17	54.8	22	16	US-09-259-943-25
C 20	17	54.8	26	9	US-08-521-634-8
C 21	14	45.2	22	1	PCT-US99-07886-52
C 22					Sequence 22, Appl
C 23					Sequence 18, Appl
C 24					Sequence 23, Appl
C 25					Sequence 23, Appl
C 26					Sequence 22, Appl
C 27					Sequence 18, Appl
C 28					Sequence 40, Appl
C 29					Sequence 22, Appl
C 30					Sequence 22, Appl
C 31					Sequence 22, Appl
C 32					Sequence 44, Appl
C 33					Sequence 29, Appl
C 34					Sequence 29, Appl
C 35					Sequence 28, Appl
C 36					Sequence 47, Appl
C 37					Sequence 29, Appl
C 38					Sequence 34, Appl
C 39					Sequence 34, Appl
C 40					Sequence 60, Appl
C 41					Sequence 25, Appl
C 42					Sequence 8, Appl
C 43					Sequence 52, Appl

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30 13 41.9 20 23 US-09-601-267-34
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32 13 41.9 25 1 PCT-US02-25940-81888
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ALIGNMENTS

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RESULT 1
US-08-272-102-22/c
; Sequence 22, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William W
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-22

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Query Match 71.0%; Score 22; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.068;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 22 CTCCTCCGCGCGCTGTTTCTC 1
RESULT 2
US-08-387-524-18/c
; Sequence 18, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-524-18

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Query Match 71.0%; Score 22; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1
RESULT 3
US-08-472-802A-23/c
; Sequence 23, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli

```

APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802A-23

Query Match 71.0%; Score 22; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 4

US-08-472-802B-23/c
Sequence 23, Application US/08472802B
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,802B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802B-23

Query Match 71.0%; Score 22; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 5

US-08-482-115A-22/c
Sequence 22, Application US/08482115A
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115A-22

Query Match 71.0%; Score 22; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 6
US-08-520-550-18/c
Sequence 18, Application US/08520550
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSH94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550-18

Query Match 71.0%; Score 22; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

US-08-521-634-40/c
Sequence 40, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-521-634-40

Query Match 71.0%; Score 22; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 8
US-08-660-678-22/c
Sequence 22, Application US/08660678


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; GENERAL INFORMATION:
; APPLICANT: VILLEPONTIEU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/660,678
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678-22

Query Match 71.0%; Score 22; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGCCGCGCGCTGTTTTCTC 22
DB 22 CTCGCCGCGCGCTGTTTTCTC 1

RESULT 9
US-09-057-351-22/c
; Sequence 22, Application US/09057351
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-22

Query Match 71.0%; Score 22; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGCCGCGCGCTGTTTTCTC 22
DB 22 CTCGCCGCGCGCTGTTTTCTC 1

RESULT 10
US-09-259-943-44/c
; Sequence 44, Application US/09259943
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A.B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; FILE REFERENCE: CSHL94-05A7
; CURRENT APPLICATION NUMBER: US/09/259,943
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/623,166
; EARLIER FILING DATE: 1996-03-28
; EARLIER APPLICATION NUMBER: 08/520,550
; EARLIER FILING DATE: 1995-08-29
; EARLIER APPLICATION NUMBER: 08/485,778
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/387,524
; EARLIER FILING DATE: 1995-02-13
; EARLIER APPLICATION NUMBER: 08/330,123
; EARLIER FILING DATE: 1994-10-27
; EARLIER APPLICATION NUMBER: 08/272,102
; EARLIER FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 30
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotides
US-09-259-943-44

Query Match          71.0%; Score 22; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 11
US-08-472-802A-29/c
; Sequence 29, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-29

Query Match          67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 21
Db 21 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 12
US-08-472-802A-29/c
; Sequence 29, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-29

Query Match          67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 21
Db 21 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 13
US-08-482-115A-28/c
; Sequence 28, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; Sequence 29, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-29

Query Match          67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCTC 21
Db 21 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 13
US-08-482-115A-28/c
; Sequence 28, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115A-28

Query Match 67.7%; Score 21; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 14
US-08-521-634-47/c
Sequence 47, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELEPHONE: (415) 326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-47

Query Match 67.7%; Score 21; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 15
US-09-057-351-29/c
Sequence 29, Application US/09057351
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H. Telomerase
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs

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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-29
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Query Match 67.7%; Score 21; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTCGCCGCGCTGTTTCT 21
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Db 21 CTCGCCGCGCTGTTTCT 1
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Job time : 1340.69 secs
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:29:49 ; Search time 377.636 Seconds
(without alignments)
120.460 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTCGTGACTTT 31

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	10	US-09-057-351-22 Sequence 22, Appl
C 2	21	67.7	28	10	US-09-057-351-29 Sequence 29, Appl
C 3	12	38.7	19	10	US-09-969-373-3585 Sequence 3585, Ap
C 4	12	38.7	20	9	US-09-932-367A-36 Sequence 36, Appl
C 5	12	38.7	25	9	US-09-992-665-170 Sequence 170, Appl
C 6	12	38.7	25	9	US-10-098-263B-48907 Sequence 48907, A
C 7	12	38.7	28	9	US-09-932-367A-89 Sequence 98, Appl
C 8	12	38.7	28	9	US-09-932-367A-98 Sequence 98, Appl
C 9	12	38.7	43	9	US-09-944-160-17 Sequence 17, Appl
C 10	11	35.5	21	9	US-10-175-225-84 Sequence 84, Appl
C 11	11	35.5	25	9	US-10-098-263B-15754 Sequence 15754, A
C 12	11	35.5	25	9	US-10-098-263B-18868 Sequence 18868, A
C 13	11	35.5	25	9	US-10-098-263B-36074 Sequence 36074, A
C 14	11	35.5	25	9	US-10-098-263B-47761 Sequence 47761, A
C 15	11	35.5	25	9	US-10-098-263B-48908 Sequence 48908, A
C 16	11	35.5	25	9	US-10-098-263B-54070 Sequence 54070, A
C 17	11	35.5	25	9	US-10-098-263B-60378 Sequence 60378, A
C 18	11	35.5	25	9	US-10-098-263B-63628 Sequence 63628, A
C 19	11	35.5	25	9	US-10-098-263B-118879 Sequence 118879, A

20	11	35.5	25	9	US-10-098-263B-118880	Sequence 118880,
C 21	11	35.5	25	9	US-10-098-263B-120100	Sequence 120100,
C 22	11	35.5	25	9	US-10-098-263B-121313	Sequence 121313,
C 23	11	35.5	25	9	US-10-098-263B-121314	Sequence 121314,
C 24	11	35.5	29	9	US-09-932-367A-84	Sequence 84, Appl
C 25	11	35.5	31	9	US-09-870-759-145	Sequence 145, Appl
C 26	11	35.5	35	9	US-10-001-189-12	Sequence 12, Appl
C 27	11	35.5	40	9	US-09-769-787-385	Sequence 84, Appl
C 28	11	35.5	40	10	US-09-245-802-84	Sequence 129, Appl
C 29	11	35.5	40	10	US-09-245-802-129	Sequence 40, Appl
C 30	10	32.3	18	10	US-09-870-162A-40	Sequence 2, Appl
C 31	10	32.3	19	10	US-09-018-125-2	Sequence 18, Appl
C 32	10	32.3	20	9	US-09-909-595-18	Sequence 51, Appl
C 33	10	32.3	20	9	US-10-238-443-42	Sequence 76, Appl
C 34	10	32.3	20	9	US-10-016-149-51	Sequence 6, Appl
C 35	10	32.3	20	9	US-09-953-318-76	Sequence 7, Appl
C 36	10	32.3	20	10	US-09-810-560-6	Sequence 237, Appl
C 37	10	32.3	21	9	US-10-090-011-7	Sequence 54, Appl
C 38	10	32.3	21	9	US-10-044-692-237	Sequence 543, Appl
C 39	10	32.3	21	9	US-10-044-539-237	Sequence 543, Appl
C 40	10	32.3	21	10	US-09-885-441-54	Sequence 543, Appl
C 41	10	32.3	22	9	US-09-978-295A-543	Sequence 543, Appl
C 42	10	32.3	22	9	US-09-978-697-543	Sequence 543, Appl
C 43	10	32.3	22	9	US-09-978-182A-543	Sequence 543, Appl
C 44	10	32.3	22	9	US-09-999-832A-543	Sequence 543, Appl
C 45	10	32.3	22	9	US-09-978-189-543	Sequence 543, Appl

ALIGNMENTS

RESULT 1
US-09-057-351-22/c
; Sequence 22, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-22

Query Match 71.0%; Score 22; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 2
US-09-057-351-29/c
Sequence 29, Application US/09057351
Patent No. US2001003439A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-29

Query Match 67.7%; Score 21; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0077;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCCTCCGCGCGCTGTTTCTC 21
DB 21 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 3
US-09-969-373-3585
Sequence 3585, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Eifert, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 3585
LENGTH: 19
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-3585

Query Match 38.7%; Score 12; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TCTCGCTGACTT 30
DB 1 TCTCGCTGACTT 12

RESULT 4
US-09-932-367A-36/c
Sequence 36, Application US/09932367A
Publication No. US20030027152A1
GENERAL INFORMATION:
APPLICANT: RHODES, Simon J.
APPLICANT: BRIDWELL, Jeanne L.
APPLICANT: MEIER, Bradley C.
APPLICANT: PARKER, Gretchen E.
APPLICANT: PRICE, Jeffrey R.
APPLICANT: SHOWALTER, Aaron D.
APPLICANT: SLOOP, Kyle W.
TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
TITLE OF INVENTION: LHX3/P-LIM/LIM-3 FACTOR
FILE REFERENCE: 053884-5003
CURRENT APPLICATION NUMBER: US/09/932,367A
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US00/04424
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/121,110
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-932-367A-36

Query Match 38.7%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 18 CTCCTCCGCGCGC 7

RESULT 5

US-09-992-665-170/c
 ; Sequence 170, Application US/09992665
 ; Publication No. US20030092009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaia Palm
 ; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ; FILE REFERENCE: CEMINS.002A
 ; CURRENT APPLICATION NUMBER: US/09/992,665
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: 60/249,508
 ; PRIOR FILING DATE: 2000-11-16
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 170
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-09-992-665-170

Query Match 38.7%; Score 12; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 23 CTCCTCCGCGCGC 12

RESULT 6

US-10-098-263B-48907
 ; Sequence 48907, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 48907
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-48907

Query Match 38.7%; Score 12; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTTTCTCGCT 25
 Db 13 GTTTTCTCGCT 24

RESULT 7

US-09-932-367A-89/c
 ; Sequence 89, Application US/09932367A
 ; Publication No. US20030027152A1
 ; GENERAL INFORMATION:

; APPLICANT: RHODES, Simon J.
 ; APPLICANT: BRIDWELL, Jeanne L.
 ; APPLICANT: MEIER, Bradley C.
 ; APPLICANT: PARKER, Gretchen E.
 ; APPLICANT: PRICE, Jeffrey R.
 ; APPLICANT: SHOWALTER, Aaron D.
 ; APPLICANT: SLOOP, Kyle W.
 ; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
 ; FILE REFERENCE: LHX3/P-LIM/LIM-3 FACTOR
 ; CURRENT APPLICATION NUMBER: US/09/932,367A
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/04424
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/121,110
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 89
 ; LENGTH: 28
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
 US-09-932-367A-89

Query Match 38.7%; Score 12; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 26 CTCCTCCGCGCGC 15

RESULT 8

US-09-932-367A-98/c
 ; Sequence 98, Application US/09932367A
 ; Publication No. US20030027152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODES, Simon J.
 ; APPLICANT: BRIDWELL, Jeanne L.
 ; APPLICANT: MEIER, Bradley C.
 ; APPLICANT: PARKER, Gretchen E.
 ; APPLICANT: PRICE, Jeffrey R.
 ; APPLICANT: SHOWALTER, Aaron D.
 ; APPLICANT: SLOOP, Kyle W.

; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
 ; FILE REFERENCE: 053884-5003
 ; CURRENT APPLICATION NUMBER: US/09/932,367A
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/04424
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/121,110
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 98
 ; LENGTH: 28
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
 US-09-932-367A-98

Query Match 38.7%; Score 12; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 26 CTCCTCCGCGCGC 15

```

RESULT 9
US-09-944-160-17/c
; Sequence 17, Application US/09944160
; Patent No. US20020174452A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. US20020174452Alman
; APPLICANT: Davin, Laurence
; APPLICANT: .. Huang, Ning
; TITLE OF INVENTION: Monocot Seeds with Increased Lignan
; FILE REFERENCE: WSUR117983
; CURRENT APPLICATION NUMBER: US/09/944,160
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/230,632
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-944-160-17

Query Match      38.7%; Score 12; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTTTTTCTCG 23
DB 32 CTGTTTTTCTCG 21

RESULT 10
US-10-175-225-84/c
; Sequence 84, Application US/10175225
; Publication No. US20030082582A1
; GENERAL INFORMATION:
; APPLICANT: Richard A. Gatti
; TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
; TITLE OF INVENTION: TELANGIECTASIA MUTATIONS
; FILE REFERENCE: UC078.001DVI
; CURRENT APPLICATION NUMBER: US/10/175,225
; CURRENT FILING DATE: 2002-08-23
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Human
US-10-175-225-84

Query Match      35.5%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTTTTTCT 21
DB 19 GCTGTTTTTCT 9

RESULT 11
US-10-098-263B-15754
; Sequence 15754, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTTTTCTCG 23
DB 13 TGTGTTTTCTCG 23

FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 15754
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-15754

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTTTTCTCG 23
DB 13 TGTGTTTTCTCG 23

RESULT 12
US-10-098-263B-18868/c
; Sequence 18868, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18868
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-18868

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTCTCGCTG 26
DB 22 TTTTCTCGCTG 12

RESULT 13
US-10-098-263B-36074
; Sequence 36074, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 36074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-36074

Query Match      35.5%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTCTCGCTG 26
DB 22 TTTTCTCGCTG 12

```


Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGCTG 14
 Db 5 CCGCGCGCTG 15

RESULT 14

US-10-098-263B-47761/c
 ; Sequence 47761, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 47761
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-47761

Query Match 35.5%; Score 11; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred.No. 3.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CTCGCTGACTT 30
 Db 18 CTCGCTGACTT 8

RESULT 15

US-10-098-263B-48908
 ; Sequence 48908, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 48908
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-48908

Query Match 35.5%; Score 11; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred.No. 3.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTTTCTCGCT 25
 Db 14 TTTTCTCGCT 24

Search completed: June 24, 2003, 20:39:36
 Job time : 378.636 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 19:12:24 ; Search time 29.719 Seconds
(without alignments)
319.896 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCGTGTTCCTGCTGACTTT 31

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B-COMB.seq.*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	1 US-08-330-123A-22	Sequence 22, Appl
C 2	22	71.0	30	1 US-08-482-115B-22	Sequence 22, Appl
C 3	22	71.0	30	2 US-08-660-678A-22	Sequence 22, Appl
C 4	22	71.0	30	2 US-08-485-778-18	Sequence 18, Appl
C 5	22	71.0	30	2 US-08-472-802C-23	Sequence 23, Appl
C 6	22	71.0	30	3 US-08-520-550A-18	Sequence 18, Appl
C 7	22	71.0	30	3 US-08-998-443-22	Sequence 22, Appl
C 8	22	71.0	30	4 US-09-060-523-22	Sequence 22, Appl
C 9	22	71.0	30	4 US-09-580-517-22	Sequence 22, Appl
C 10	21	67.7	28	1 US-08-482-115B-28	Sequence 28, Appl
C 11	21	67.7	28	2 US-08-472-802C-29	Sequence 29, Appl
C 12	21	67.7	30	2 US-08-485-778-34	Sequence 34, Appl
C 13	21	67.7	30	3 US-08-520-550A-34	Sequence 34, Appl
C 14	12	38.7	20	1 US-08-089-996-21	Sequence 21, Appl
C 15	12	38.7	20	1 US-08-089-996-22	Sequence 22, Appl
C 16	12	38.7	20	2 US-08-478-178A-21	Sequence 21, Appl
C 17	12	38.7	20	2 US-08-478-178A-22	Sequence 22, Appl
C 18	12	38.7	20	2 US-08-488-177-21	Sequence 21, Appl
C 19	12	38.7	20	2 US-08-488-177-22	Sequence 22, Appl
C 20	12	38.7	20	2 US-08-481-072A-21	Sequence 21, Appl
C 21	12	38.7	20	2 US-08-481-072A-22	Sequence 22, Appl
C 22	12	38.7	20	2 US-08-664-336-21	Sequence 21, Appl
C 23	12	38.7	20	2 US-08-664-336-22	Sequence 22, Appl
C 24	12	38.7	20	2 US-08-481-066A-21	Sequence 21, Appl
C 25	12	38.7	20	2 US-08-481-066A-22	Sequence 22, Appl
C 26	12	38.7	20	3 US-08-578-615A-21	Sequence 21, Appl
C 27	12	38.7	20	3 US-08-578-615A-22	Sequence 22, Appl

C 28	12	38.7	20	4 US-08-829-637A-21	Sequence 21, Appl
C 29	12	38.7	20	4 US-08-829-637A-22	Sequence 22, Appl
C 30	12	38.7	20	4 US-09-254-322-21	Sequence 21, Appl
C 31	12	38.7	20	4 US-09-254-322-22	Sequence 22, Appl
C 32	12	38.7	20	5 PCT-US93-02213-21	Sequence 21, Appl
C 33	12	38.7	20	5 PCT-US93-02213-22	Sequence 22, Appl
C 34	12	38.7	20	5 PCT-US94-07770-21	Sequence 21, Appl
C 35	12	38.7	20	5 PCT-US94-07770-22	Sequence 22, Appl
C 36	12	38.7	22	4 US-08-564-989-8	Sequence 8, Appl
C 37	11	35.5	20	1 US-08-534-975-12	Sequence 12, Appl
C 38	11	35.5	20	2 US-08-954-470-12	Sequence 12, Appl
C 39	11	35.5	20	3 US-09-129-855A-12	Sequence 12, Appl
C 40	11	35.5	20	4 US-09-444-053-39	Sequence 39, Appl
C 41	11	35.5	20	4 US-09-247-154-12	Sequence 12, Appl
C 42	11	35.5	20	4 US-09-306-405-68	Sequence 68, Appl
C 43	11	35.5	20	4 US-09-480-718-12	Sequence 12, Appl
C 44	11	35.5	21	1 US-08-753-147-65	Sequence 65, Appl
C 45	11	35.5	21	4 US-09-360-416-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-08-330-123A-22/c
; Sequence 22, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/330,123A
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-22

Query Match 71.0%; Score 22; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTTTCTC 1

RESULT 2

US-08-482-115B-22/c
; Sequence 22, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-22

Query Match 71.0%; Score 22; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTTTCTC 1

RESULT 3

US-08-660-678A-22/c
; Sequence 22, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-22

Query Match 71.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCCGCGCGCTGTTTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTTTCTC 1

RESULT 4

US-08-485-778-18/c
; Sequence 18, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-18

Query Match 71.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTTCTC 1

RESULT 5
US-08-472-802C-23/c
Sequence 23, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Vilponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-23

Query Match 71.0%; Score 22; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTTCTC 1

RESULT 6
US-08-520-550A-18/c
Sequence 18, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Vilponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-18

Query Match 71.0%; Score 22; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 7
US-08-998-443-22/c
; Sequence 22, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

Query Match 71.0%; Score 22; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 8
US-09-060-523-22/c
; Sequence 22, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

Query Match 71.0%; Score 22; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 9
US-09-580-517-22/c
; Sequence 22, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-580-517-22

Query Match 71.0%; Score 22; DB 4; Length 30;
Best Local Similarity: 100.0%; Pred. No. 0.0016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCCTCCGCGCGCTGTTTCTC 22
DB 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 10
US-08-482-115B-28/c
Sequence 28, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-28

Query Match 67.7%; Score 21; DB 1; Length 28;
Best Local Similarity: 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTCCTCCGCGCGCTGTTTCTC 21
DB 21 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 11
US-08-472-802C-29/c
Sequence 29, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-29

Query Match 67.7%; Score 21; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTGGCGCTGTTTCT 21
DB 21 CTCCTGGCGCTGTTTCT 1

RESULT 12

US-08-485-778-34
; Sequence 34, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-485-778-34

Query Match 67.7%; Score 21; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QX 9 GCGCTGTTTCTCGCTGACT 29

DB 10 GCGCTGTTTCTCGCTGACT 30

RESULT 13

US-08-520-550A-34
; Sequence 34, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-34

Query Match 67.7%; Score 21; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCTGTTTCTCGCTGACT 29
DB 10 GCGCTGTTTCTCGCTGACT 30

RESULT 14

US-08-089-996-21/c
; Sequence 21, Application US/08089996
; Patent No. 5703054
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett

;; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & No. 5703054ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/089,996
;; FILING DATE: 19930709
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 852,852
;; FILING DATE: March 16, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rebecca Ralph Gaumont
;; REGISTRATION NUMBER: 35,152
;; REFERENCE/DOCKET NUMBER: ISIS-1154
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: yes
US-08-089-996-21

Query Match 38.7%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
Db 18 CTCCTCCGCGCGC 7

RESULT 15
US-08-089-996-22/c
;; Sequence 22, Application US/08089996
;; Patent No. 5703054
;; GENERAL INFORMATION:
;; APPLICANT: Nicholas Dean, C. Frank Bennett
;; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & No. 5703054ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/089,996
;; FILING DATE: 19930709

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 852,852
;; FILING DATE: March 16, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rebecca Ralph Gaumont
;; REGISTRATION NUMBER: 35,152
;; REFERENCE/DOCKET NUMBER: ISIS-1154
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: yes
US-08-089-996-22

Query Match 38.7%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
Db 13 CTCCTCCGCGCGC 2

Search completed: June 24, 2003, 16:54:55
Job time : 30.719 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:14:29 ; Search time 117.339 Seconds
(without alignments)
594.960 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTTCGCTGACTTT 31

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*	
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*	
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	71.0	30	17 AAT10298	RNA component of h
C 2	22	71.0	30	17 AAT1043	Primer for product
C 3	21	67.7	30	17 AAT11059	Primer used for am
C 4	14	45.2	22	20 AAZ33130	Treponema pallidum
C 5	13	41.9	20	20 AAZ07291	Mouse telomerase R
C 6	13	41.9	20	20 AAZ07294	Mouse telomerase R
C 7	13	41.9	22	21 AAZ29625	Tick derived cyste
C 8	13	41.9	28	24 ABL60273	Borrelia burgdorfe
C 9	13	41.9	29	20 AAZ07292	Mouse telomerase R

ALIGNMENTS

RESULT 1

AAAT10298/c	
ID AAT10298 standard; DNA; 30 BP.	
XX AC AAT10298;	
XX DT 09-SEP-1996 (first entry)	
XX DE RNA component of human telomerase antisense plasmid PCR primer G1.	
XX DE RNA component; human; telomerase; lung fibroblast; cell line WI-38;	
KW recombinant production; synthesis; mutant; detection; mammalian;	
KW identification; modulating agent; neoplastic condition;	
KW transcriptional regulatory sequence; gene therapy; disease;	
KW polymerase chain reaction; antisense plasmid; PCR primer; ss.	
XX OS Synthetic.	
XX PN WO9601835-A1.	
XX PD 25-JAN-1996.	
XX PF 06-JUL-1995; 95WO-US08530.	
XX PR 07-JUN-1995; 95US-0482115.	
XX PR 07-JUL-1994; 94US-0272102.	
XX PR 27-OCT-1994; 94US-0330123.	
XX PR 07-JUN-1995; 95US-0472802.	
XX PA (GERO-) GERON CORP.	
XX PA Andrews WH, Feng J, Funk W, Villeponteau B;	
XX PI	

Galanin receptor g
Galanin receptor g
Galanin receptor g
PKC-beta type I an
PKC-beta type I an
PKC-beta type I an
PNA oligomer targe
PNA oligomer targe
PKC-beta type I an
PKC-beta type I an
PKC-beta type I an
Oligo ON21 targete
Oligo ON22 targete
Human protein kina
Human protein kina
Human PKC-beta typ
Human PKC-beta typ
Human PKC-beta typ
Mammalian Lhx3 PCR
Human protein kina
Human protein kina
Human protein kina
Human PKC-beta typ
Human PKC-beta typ
Human PKC-beta typ
Human Lhx3 PCR pri
Human Lhx3 PCR pri
Human Lhx3 PCR pri
PCR primer used to
Oligonucleotide pr
Galanin receptor g
Galanin receptor g
Hammerhead ribozym
Human cdc37 nuclei
cdk6 ribozyme bind
Cell-cycle depende

XX WPI; 1996-097581/10.
 XX RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents
 XX
 XX Example 8; Page 80; 114pp; English.
 CC The present sequence is a PCR primer for a RNA component of human
 CC telomerase (RCHT), antisense plasmid. RCHT was derived from a
 CC genomic DNA library obtd. from the human lung fibroblast cell line
 CC WI-38. The RCHT can be used in the recombinant prodn. of an active
 CC telomerase mol., capable of adding sequences to chromosomal DNA
 CC telomeres, and in the synthesis of mutant sequences for the
 CC detection of mutant mammalian telomerase RNA component
 CC polynucleotides. The RCHT may also be used in the identification
 CC of telomerase modulating agents, and in the detection of
 CC telomerase related, or neoplastic conditions in a patient.
 CC Polynucleotides of at least 25 consecutive nucleotides identical,
 CC or complementary to the RCHT sequence linked to heterologous
 CC transcriptional regulatory sequences, can be used for the gene
 CC therapy of human diseases.
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 11 G; 0 U; 0 other;
 Query Match 71.0%; Score 22; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCGCGCTGTTTCTC 22
 |||||
 DB 22 CTCCTCCGCGCGCTGTTTCTC 1
 RESULT 2
 AAT11043/c
 ID AAT11043 standard; DNA; 30 BP.
 AC AAT11043;
 XX
 DT 02-JUL-1996 (first entry)
 DE Primer for production of telomerase antisense oligonucleotide.
 XX
 KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KW plasmid; probe; primer; ribozyme; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601614-A2.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US08620.
 XX
 PR 07-JUN-1995; 95US-0485778.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 13-FEB-1995; 95US-0387524.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (GERO-) GERON CORP.
 XX
 PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
 PI Marhuenda MA, Villeponteau B;
 XX
 WPI; 1996-097428/10.
 XX
 RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 XX
 XX Example 1; Page 53; 85pp; English.

CC The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the
 CC telomerase gene (also claimed) can be used for study of telomere
 CC regulation in vivo, and the role it plays in immortalisation.
 CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
 CC antisense oligonucleotides which were then used to produce antisense
 CC expression plasmids. AAT11040 was used alongside both AAT11043 and
 CC AAT11044 to produce two different antisense molecules.
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 11 G; 0 U; 0 other;
 Query Match 71.0%; Score 22; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCCTCCGCGCGCTGTTTCTC 22
 |||||
 DB 22 CTCCTCCGCGCGCTGTTTCTC 1
 RESULT 3
 AAT11059
 ID AAT11059 standard; DNA; 30 BP.
 XX
 AC AAT11059;
 XX
 DT 02-JUL-1996 (first entry)
 DE Primer used for amplifying telomerase RNA fragments.
 XX
 KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KW plasmid; probe; primer; ribozyme; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601614-A2.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US08620.
 XX
 PR 07-JUN-1995; 95US-0485778.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 13-FEB-1995; 95US-0387524.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (GERO-) GERON CORP.
 XX
 PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
 PI Marhuenda MA, Villeponteau B;
 XX
 WPI; 1996-097428/10.
 XX
 RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 XX
 XX Example 15; Page 60; 85pp; English.
 CC The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the

CC telomerase gene (also claimed) can be used for study of telomere regulation in vivo, and the role it plays in immortalisation.
 CC Four primers (AAT11057, AAT11058 and AAT11059, AAT11060) which are complementary to human telomerase RNA component sequences can be used to identify and amplify homologous sequences from other CC non-human mammals. The amplified fragments can then be used as CC probes to identify telomerase genes.
 XX Sequence 30 BP; 3 A; 9 C; 7 G; 11 T; 0 other;
 SQ Query Match 67.7%; Score 21; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCGCTGTTTCTCGCTGACT 29
 Db 10 GCGCTGTTTCTCGCTGACT 30
 RESULT 4
 AA233130
 ID AA233130 standard; DNA; 22 BP.
 AC AA233130;
 XX 26-JAN-2000 (first entry)
 DT Treponema pallidum Msp variable region sense PCR primer S7.
 DE Treponema pallidum; syphilis; vaccine; treponemal disease; Msp;
 KW major sheath protein; bejal; gingivitis; periodontal disease; pinta;
 KW yaws; PCR primer; ss.
 XX Synthetic.
 OS Treponema pallidum.
 XX WO9953099-A1.
 PN 21-OCT-1999.
 PD 09-APR-1999; 99WO-US07886.
 PF 10-APR-1998; 98US-0058968.
 PR (UNIW) UNIV WASHINGTON.
 PA Van Voorhis.WC, Lukehart SA, Centurion-Lara GA, Cameron CES;
 PI WPI; 1999-620445/53.
 XX Novel proteins useful in vaccines against syphilis and other treponemal diseases -
 PT Claim 3; Page 86; 200pp; English.
 PS The present invention describes novel Treponema pallidum genes. These CC genes encode a glycerophosphodiester phosphodiesterase (Gpd), a CC D15/Oma87 homologue, and proteins with homology to major outer sheath CC (Msp) proteins of T. denticola. Also described are: (1) an isolated CC protein capable of inducing a protective immunologic response to CC T. p. pallidum, T. p. pertenue, or T. p. endemicum, when administered CC in an effective amount to an animal host; (2) a method of identifying CC a T. p. pallidum vaccine candidate; (3) a method of inducing a CC protective immune response against T. pallidum; (4) a method for CC analysing a sample of DNA to determine whether it originated from CC T. p. subspecies pallidum, T. p. subspecies pertenue or T. p. subspecies CC endemicum; and (5) a method of determining whether a first and a second CC clinical isolate of T. p. pallidum are the same or different. The CC proteins are used, either alone or in combination, in vaccines against CC Treponemal diseases, e.g. syphilis, bejal, pinta, yaws, gingivitis, CC and periodontal disease. They may also provide protection against CC other treponemal diseases. The methods may be used to identify vaccine CC candidates, and to determine the origin of a treponemal nucleic acid.

CC AA233104 to AA233156, and AA252773 to AA252831, represent sequences used CC in the exemplification of the present invention.
 XX Sequence 22 BP; 1 A; 6 C; 4 G; 11 T; 0 other;
 SQ Query Match 45.2%; Score 14; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 TTTTCTCGCTGAC 28
 Db 2 TTTTCTCGCTGAC 15
 RESULT 5
 AA207291/c
 ID AA207291 standard; DNA; 20 BP.
 XX AA207291;
 AC AA207291;
 XX 22-OCT-1999 (first entry)
 DT Mouse telomerase RNA gene specific primer mTRr1.
 DE Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
 KW gene therapy; thymidine kinase gene; anticancer therapy; mouse;
 KW PCR primer; ss.
 XX Synthetic.
 OS Mus sp.
 XX WO9938964-A2.
 PN 05-AUG-1999.
 PD 29-JAN-1999; 99WO-GB00308.
 PF 29-JAN-1998; 98GB-0001902.
 PR (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA Keith WN;
 PI WPI; 1999-479183/40.
 XX Mouse and human telomerase RNA gene promoters, useful for tumor specific gene therapy
 PT Disclosure; Fig 6; 109pp; English.
 PS The invention relates to promoter regions from mouse and human CC telomerase RNA (TR) component genes. The TR gene promoter can be linked CC to a heterologous gene, especially a gene encoding a cytotoxin, for CC therapy of cancer, especially neoplasias. The telomerase is necessary for CC the unrestricted proliferative capacity of many human cancers. Mutation CC or dysregulation of the telomerase repression pathway may cause CC Substances, identified in the methods, can be used to block transcription CC from the TR gene promoter through interaction of the 5' regulatory CC sequences. These substances, e.g. antisense oligonucleotides, CC transcription factors, peptide nucleic acids and factors that disrupt CC signal transduction, are useful for cancer therapy. In particular, gene CC therapy vectors (especially pGT62-codAupp) comprising the promoter and a CC viral thymidine kinase gene can be used to convert a prodrug, e.g. CC gancyclovir, so that neoplasia can be controlled or treated. Direct CC down-regulation of telomerase RNA gene through manipulation of CC transcription factors may be effective anticancer therapy and the cloning CC of the HTR gene promoter allows the analysis of therapeutic molecules CC which modulate HTR promoter activity. Sequences AA207681-95 represent PCR CC primers for amplifying mouse TR gene (terc) promoter sequence.
 XX Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;

Query Match 41.9%; Score 13; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTCTCGCTGACTT 30
 DB 20 TTCTCGCTGACTT 8

RESULT 6

AAZ07294/c
 ID AAZ07294 standard; DNA; 20 BP.
 AC AAZ07294;
 XX
 DT 22-OCT-1999 (first entry)
 DE Mouse telomerase RNA gene specific primer mTR1.
 XX
 KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
 KW gene therapy; thymidine kinase gene; anticancer therapy; mouse;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9938964-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 29-JAN-1999; 99WO-GB00308.
 XX
 PR 29-JAN-1998; 98GB-0001502.
 XX
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Keith WN;
 XX
 WPI; 1999-479183/40.
 DR
 XX
 PT Mouse and human telomerase RNA gene promoters, useful for tumor
 PT specific gene therapy
 XX
 PS Disclosure; Fig 6; 109pp; English.
 XX
 CC The invention relates to promoter regions from mouse and human
 CC telomerase RNA (TR) component genes. The TR gene promoter can be linked
 CC to a heterologous gene, especially a gene encoding a cytotoxin, for
 CC therapy of cancer, especially neoplasias. The telomerase is necessary for
 CC the unrestricted proliferative capacity of many human cancers. Mutation
 CC or dysregulation of the telomerase repression pathway may cause
 CC reactivation or upregulation of telomerase expression in cancer.
 CC Substances, identified in the methods, can be used to block transcription
 CC from the TR gene promoter through interaction of the 5' regulatory
 CC sequences. These substances, e.g. antisense oligonucleotides,
 CC transcription factors, peptide nucleic acids and factors that disrupt
 CC signal transduction, are useful for cancer therapy. In particular, gene
 CC therapy vectors (especially pGT62-codAupp) comprising the promoter and a
 CC viral thymidine kinase gene can be used to convert a prodrug, e.g.
 CC gancyclovir, so that neoplasia can be controlled or treated. Direct
 CC down-regulation of telomerase RNA gene through manipulation of
 CC transcription factors may be effective anticancer therapy and the cloning
 CC of the hTR gene promoter allows the analysis of therapeutic molecules
 CC which modulate hTR promoter activity. Sequences AAZ07681-95 represent PCR
 CC primers for amplifying mouse TR gene (terc) promoter sequence.
 XX
 XX Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;

Query Match 41.9%; Score 13; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTCTCGCTGACTT 30

Db 20 TTCTCGCTGACTT 8

RESULT 7
 AAA29625
 ID AAA29625 standard; DNA; 22 BP.
 XX
 AC AAA29625;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Tick derived cysteine protease primer PR-2.
 XX
 KW Tick; vaccine; infection; salivary gland antigen; immunogen;
 KW serine protease; cysteine protease; blood sucker; primer; ss.
 XX
 OS Haemaphysalis longicornis.
 XX
 PN JP2000083677-A.
 XX
 PD 28-MAR-2000.
 XX
 PF 17-SEP-1998; 98JP-0281932.
 XX
 PR 17-SEP-1998; 98JP-0281932.
 XX
 PA (FARB) BAYER KK.
 XX
 DR WPI; 2000-296340/26.
 XX
 PT A gene encoding tick salivary gland antigen - useful as a vaccine for
 PT protecting animals from tick-carried infections
 XX
 PS Example 7; Page 15; 29pp; Japanese.
 XX
 CC The present sequence represents a primer used in the isolation of a tick
 CC derived cysteine protease. The present invention also describes a tick
 CC salivary gland antigen related immunogen and a tick derived serine
 CC protease. A nucleotide sequence encoding any of the above proteins can
 CC be used in a vaccine against tick carried infections for domestic
 CC animals such as cattle.
 XX
 SQ Sequence 22 BP; 3 A; 7 C; 4 G; 8 T; 0 other;

Query Match 41.9%; Score 13; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTTTTCTCG 23
 DB 4 GCTGTTTTCTCG 16

RESULT 8
 ABL60273/c
 ID ABL60273 standard; DNA; 28 BP.
 XX
 AC ABL60273;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Borrelia burgdorferi ZS7 ospA PCR primer 1.
 DE
 KW Lyme disease; spirochete; antibacterial; Borrelia; infection; vaccine;
 KW Lyme borreliosis; veterinary; PCR; primer; ospA; ss.
 XX
 OS Borrelia burgdorferi.
 XX
 PN DE10126367-A1.
 XX
 PD 23-MAY-2002.
 XX

PF 30-MAY-2001; 2001DE-1026367.
 XX
 PR 20-NOV-2000; 2000DE-1057442.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Simon MM, Wallich R;
 XX
 XX WPI; 2002-445465/48.
 DR
 XX Pharmaceutical composition comprises Borrelia antigens and encoding
 PT nucleic acid, useful for diagnosis, treatment and prevention of Lyme
 PT borreliosis .
 XX
 PS Example 1; Page 6; 58pp; German.
 XX
 XX The invention relates to a pharmaceutical composition comprising at least
 CC one of: (a) a polypeptide (I) comprising fully defined sequences of
 CC ABB77511, ABB77512, ABB77514 or ABB77521 or the corresponding polypeptide
 CC from other Borrelia or their immunogenic fragments; (b) nucleic acids
 CC (ii) that encode (I) or sequences that hybridise with them under
 CC stringent conditions; or (c) antibodies directed against (I). The
 CC antibodies are used for diagnosis of Borrelia infection (Lyme
 CC borreliosis) and in vaccines for Borrelia infection (Lyme
 CC infections), in human or veterinary medicine. The present sequence is that
 CC of a PCR primer for amplification of a Borrelia burgdorferi
 CC polynucleotide sequence of the invention.
 XX
 SQ Sequence 28 BP; 10 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 41.9%; Score 13; DB 24; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GCTGTTTCTCG 23
 DB 28 GCTGTTTCTCG 16
 RESULT 9
 AAZ07292/c
 ID AAZ07292 standard; DNA; 29 BP.
 XX
 AC AAZ07292;
 XX
 XX 22-OCT-1999 (first entry)
 DT
 XX
 DE Mouse telomerase RNA gene specific primer mtr30r.
 XX
 KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
 KW Gene therapy; thymidine kinase gene; anticancer therapy; mouse;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9338964-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 29-JAN-1999; 99WO-GB00308.
 XX
 PR 29-JAN-1998; 98GB-0001902.
 XX
 XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA
 XX Keith WN;
 PI
 XX WPI; 1999-479183/40.
 DR
 XX Mouse and human telomerase RNA gene promoters, useful for tumor
 PT specific gene therapy
 PT
 XX

PS Disclosure; Fig 6; 109pp; English.
 XX
 CC The invention relates to promoter regions from mouse and human
 CC telomerase RNA (TR) component genes. The TR gene promoter can be linked
 CC to a heterologous gene, especially a gene encoding a cytotoxin, for
 CC therapy of cancer, especially neoplasias. The telomerase is necessary for
 CC the unrestricted proliferative capacity of many human cancers. Mutation
 CC or dysregulation of the telomerase repression pathway may cause
 CC reactivation or upregulation of telomerase expression in cancer.
 CC Substances, identified in the methods, can be used to block transcription
 CC from the TR gene promoter through interaction of the 5' regulatory
 CC sequences. These substances, e.g. antisense oligonucleotides,
 CC transcription factors, peptide nucleic acids and factors that disrupt
 CC signal transduction, are useful for cancer therapy. In particular, gene
 CC therapy vectors (especially pGT62-codAupp) comprising the promoter and a
 CC viral thymidine kinase gene can be used to convert a prodrug, e.g.
 CC gancyclovir, so that neoplasia can be controlled or treated. Direct
 CC down-regulation of telomerase RNA gene through manipulation of
 CC transcription factors may be effective anticancer therapy and the cloning
 CC of the hTR gene promoter allows the analysis of therapeutic molecules
 CC which modulate hTR promoter activity. Sequences AAZ07681-95 represent PCR
 CC primers for amplifying mouse TR gene (terc) promoter sequence.
 XX
 SQ Sequence 29 BP; 8 A; 8 C; 9 G; 4 T; 0 other;
 Query Match 41.9%; Score 13; DB 20; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 TTTCGCTGACTT 30
 DB 29 TTTCGCTGACTT 17
 RESULT 10
 AAS98334/c
 ID AAS98334 standard; DNA; 15 BP.
 XX
 AC AAS98334;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX
 DE Galanin receptor gene GALR1 allele-specific oligonucleotide #46.
 XX
 KW Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;
 KW drug discovery; haplotyping; infectious diarrhoea;
 KW growth hormone deficiency; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200179237-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US12306.
 XX
 PR 14-APR-2000; 2000US-197838P.
 XX
 XX (GENA-) GENAISANCE PHARM INC.
 PA
 XX Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
 PI
 XX WPI; 2002-066341/09.
 DR
 XX Genotyping human galanin receptor gene of an individual for determining
 PT haplotype of an individual, involves determining the identity of
 PT nucleotide pair at specific polymorphic sites for two copies of the
 PT gene .
 XX
 PS Claim 16; Page 15; 99pp; English.
 XX
 CC The invention relates to genotyping human galanin receptor (GALR1) gene
 CC of an individual, involving determining for the two copies of the GALR1

CC gene present in the individual, the identity of the nucleotide pair at
 CC one or more polymorphic sites. The method is useful for determining
 CC whether an individual has a haplotype or haplotype pairs defined in the
 CC specification. This is useful for improving the efficacy and reliability
 CC of several steps in the discovery and development of drugs for treating
 CC diseases associated with GALR1 activity, e.g., infectious diarrhoea and
 CC growth hormone deficiency, to validate GALR1 as a candidate agent for
 CC treating a specific condition or disease predicted to be associated with
 CC GALR1 activity, and in the design of clinical trials of candidate drugs
 CC for treating a specific condition or disease predicted to be associated
 CC with GALR1 activity. The method is useful to screen for compounds
 CC targeting GALR1 to treat a specific condition or disease associated
 CC with GALR1 activity. A GALR1 polynucleotide or variant is useful in
 CC studying the expression and function of GALR1, and in expressing GALR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to GALR1 activity. The polynucleotide or variant is useful for
 CC studying expression of the GALR1 isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against GALR1 protein, and for studying the
 CC effect of the variation on the biological activity of GALR1 as well as on
 CC the binding affinity of candidate drugs targeting GALR1 for the treatment
 CC of infectious diarrhoea and growth hormone insufficiency. AAS98289-
 CC AAS98408 represent human GALR1 gene allele-specific oligonucleotides used
 CC to detect GALR1 gene polymorphisms as described in the method of the
 CC invention.

XX Sequence 15 BP; 2 A; 3 C; 9 G; 0 U; 1 other;
 SQ Query Match 38.7%; Score 12; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 12 CTCCTCCGCGCGC 1

RESULT 11

AAS98336/c
 ID AAS98336 standard; DNA; 15 BP.
 XX
 AC AAS98336;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Galanin receptor gene GALR1 allele-specific oligonucleotide #48.
 XX
 KW Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;
 KW drug discovery; haplotyping; infectious diarrhoea;
 KW growth hormone deficiency; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200179237-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US12306.
 XX
 PR 14-APR-2000; 2000US-197838P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
 XX
 DR WPI; 2002-066341/09.

XX Genotyping human galanin receptor gene of an individual for determining
 PT haplotype of an individual, involves determining the identity of
 PT nucleotide pair at specific polymorphic sites for two copies of the
 PT gene -
 XX Claim 16; Page 15; 99pp; English.

CC The invention relates to genotyping human galanin receptor (GALR1) gene
 CC of an individual, involving determining for the two copies of the GALR1
 CC gene present in the individual, the identity of the nucleotide pair at
 CC one or more polymorphic sites. The method is useful for determining
 CC whether an individual has a haplotype or haplotype pairs defined in the
 CC specification. This is useful for improving the efficacy and reliability
 CC of several steps in the discovery and development of drugs for treating
 CC diseases associated with GALR1 activity, e.g., infectious diarrhoea and
 CC growth hormone deficiency, to validate GALR1 as a candidate agent for
 CC treating a specific condition or disease predicted to be associated with
 CC GALR1 activity, and in the design of clinical trials of candidate drugs
 CC for treating a specific condition or disease predicted to be associated
 CC with GALR1 activity. The method is useful to screen for compounds
 CC targeting GALR1 to treat a specific condition or disease associated
 CC with GALR1 activity. A GALR1 polynucleotide or variant is useful in
 CC studying the expression and function of GALR1, and in expressing GALR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to GALR1 activity. The polynucleotide or variant is useful for
 CC studying expression of the GALR1 isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against GALR1 protein, and for studying the
 CC effect of the variation on the biological activity of GALR1 as well as on
 CC the binding affinity of candidate drugs targeting GALR1 for the treatment
 CC of infectious diarrhoea and growth hormone insufficiency. AAS98289-
 CC AAS98408 represent human GALR1 gene allele-specific oligonucleotides used
 CC to detect GALR1 gene polymorphisms as described in the method of the
 CC invention.

XX Sequence 15 BP; 1 A; 3 C; 10 G; 0 U; 1 other;
 SQ Query Match 38.7%; Score 12; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
 Db 13 CTCCTCCGCGCGC 2

RESULT 12

AAS98341
 ID AAS98341 standard; DNA; 15 BP.
 XX
 AC AAS98341;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Galanin receptor gene GALR1 allele-specific oligonucleotide #53.
 XX
 KW Galanin receptor; GALR1; human; single nucleotide polymorphism; SNP;
 KW drug discovery; haplotyping; infectious diarrhoea;
 KW growth hormone deficiency; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200179237-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US12306.
 XX
 PR 14-APR-2000; 2000US-197838P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
 XX
 DR WPI; 2002-066341/09.

XX Genotyping human galanin receptor gene of an individual for determining
 PT haplotype of an individual, involves determining the identity of
 PT nucleotide pair at specific polymorphic sites for two copies of the
 PT gene -
 XX Claim 16; Page 15; 99pp; English.

W09319203-A.
30-SEP-1993.
25-FEB-1993; 93WO-US02213.
16-MAR-1992; 92US-0852852.
(ISIS-) ISIS PHARM INC.

XX Oligo-nucleotide(s) hybridize to nucleic acids encoding Protein
PT kinase C - useful as diagnostics and therapeutics for disease
PT states associated with particular isoforms of PKC
yx

PS Claim 6; Page 18; 64pp; English.

XX The sequences given in AAQ49657-707 are antisense oligonucleotides

CC which contain altered inter-sugar linkages, pref. phosphorothionate

CC linkages. These oligomers bind with the protein kinase C (PKC) mRNA

CC at the transcription initiation site, the translation initiation

CC or sequences in the 5'- or 3'-untranslated regions. These

CC oligonucleotides may be used in diagnostics, therapeutics,

CC prophylaxis and as research reagents. The numbers allocated to

CC on the cDNA, which is 28 residues upstream of the AUG start codon.

XX

SQ Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 other;

Query Match 38.7%; Score 12; DB 14; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 CTCCTCCGCGCGC 12

DB 13 CTCCTCCGCGCGC 2

RESULT 15

AAQ97894/c

ID AAQ97894 standard; DNA; 20 BP.

XX

AC AAQ97894;

XX

DT 17-OCT-1995 (first entry)

XX

DE PNA oligomer targetting AUG region of PKC-beta isoforms I & II.

XX

KW Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;

KW cell proliferation; cell differentiation; isozyme; antisense;

KW triple helix; cancer; psoriasis; inflammation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc_feature 1..20

FT /tag= a

FT /note= "at least one (and preferably all) of

FT the backbone subunits are composed of N-acetyl

FT N-(2-aminoethyl)glycine peptide residues, the

FT nucleobase being attached covalently to the

FT acetyl group and the peptide linkage being

FT formed by condensation of the glycine

FT carboxy group of one residue with the amino

FT group of the 2-aminoethyl moiety in the next

FT residue"

XX

PN WO9503833-A.

XX

PD 09-FEB-1995.

XX

PP 28-JUL-1994; 94WO-US08465.

XX

PR 29-JUL-1993; 93US-0099098.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Dean NM;

XX

DR WPI; 1995-082040/11.

XX

PT New peptide nucleic acid oligomers specific for protein kinase C

PT isozyme(s) - useful as anti-sense molecules for treating PKC

PT mediated disease, e.g. cancer, psoriasis and inflammation

XX

XX Claim 10; Page 261; 287pp; English.

XX

CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist

CC of naturally occurring nucleobases covalently bound to a polyamide

CC backbone and (b) hybridise to the translation initiation AUG region,

CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region

CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target

CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene

CC regulation moieties. They inhibit expression of PKC-alpha and its

CC isoforms (including beta, gamma, delta, epsilon, zeta and eta) and so

CC are useful for treating and diagnosing cell proliferation and

CC differentiation processes such as neoplastic, hyperproliferative

CC and inflammatory diseases.

CC PNA oligomers have high affinity for complementary single stranded DNA.

CC They are also able to form triple helices in which a first PNA strand

CC binds with RNA or ssDNA and a second PNA strand binds with the resulting

CC double helix or with the first PNA strand. The PNAs possess no

CC significant charge and are water soluble, which facilitates cellular

CC uptake. Further, since they contain amides of non-biological amino acids,

CC they are biostable and resistant to enzymatic degradation by proteases.

CC The present sequence targets the AUG region of PKC-beta isoforms I & II.

XX

SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;

Query Match 38.7%; Score 12; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 CTCCTCCGCGCGC 12

DB 18 CTCCTCCGCGCGC 7

Search completed: June 23, 2003, 20:09:19

Job time : 118.339 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:17:23 ; Search time 308.975 Seconds
(without alignments)
2919.933 Million cell updates/sec

Title: US-08-770-564A-1_COPY_350_380

Perfect score: 31
Sequence: 1 CTCGCCGCGCTGTTTCTTCGCTGACTTT 31

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sta.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	22	71.0	30	6	AR016054	AR016054 Sequence
C 2	22	71.0	30	6	AR059215	AR059215 Sequence
C 3	22	71.0	30	6	AR075526	AR075526 Sequence
C 4	22	71.0	30	6	AR161924	AR161924 Sequence
C 5	22	71.0	30	6	I31769	I31769 Sequence 22
C 6	21	67.7	28	6	AR016060	AR016060 Sequence
C 7	21	67.7	28	6	AR075532	AR075532 Sequence
C 8	13	41.9	20	6	AX019577	AX019577 Sequence
C 9	13	41.9	20	6	AX019580	AX019580 Sequence
C 10	13	41.9	29	6	AX019578	AX019578 Sequence
C 11	12	38.7	20	6	AR076656	AR076656 Sequence
C 12	12	38.7	20	6	AR076657	AR076657 Sequence
C 13	12	38.7	20	6	AR182713	AR182713 Sequence
C 14	12	38.7	20	6	AR182714	AR182714 Sequence
C 15	12	38.7	20	6	AX226311	AX226311 Sequence
C 16	12	38.7	20	6	AX226312	AX226312 Sequence
C 17	12	38.7	20	6	I87125	I87125 Sequence 21
C 18	12	38.7	20	6	I87126	I87126 Sequence 22
C 19	12	38.7	22	6	A51391	A51391 Sequence 7
C 20	12	38.7	25	6	E16661	E16661 PCR primer
C 21	11	35.5	18	6	A97274	A97274 Sequence 12
C 22	11	35.5	19	6	AX129365	AX129365 Sequence
C 23	11	35.5	20	6	AR122485	AR122485 Sequence
C 24	11	35.5	20	6	AR124806	AR124806 Sequence
C 25	11	35.5	20	6	AR161568	AR161568 Sequence
C 26	11	35.5	20	6	AX298535	AX298535 Sequence
C 27	11	35.5	20	6	I89927	I89927 Sequence 12
C 28	11	35.5	21	12	AB068319	AB068319 Synthetic
C 29	11	35.5	25	6	AX350093	AX350093 Sequence
C 30	11	35.5	27	6	AR039910	AR039910 Sequence
C 31	11	35.5	27	6	AR184928	AR184928 Sequence
C 32	11	35.5	27	6	AR191109	AR191109 Sequence
C 33	11	35.5	27	6	AR191441	AR191441 Sequence
C 34	11	35.5	29	6	A49464	A49464 Sequence 4
C 35	11	35.5	29	6	AR093964	AR093964 Sequence
C 36	11	35.5	30	6	AR037771	AR037771 Sequence
C 37	11	35.5	30	6	I17308	I17308 Sequence 17
C 38	11	35.5	31	6	A23777	A23777 CASOL10 oli
C 39	11	35.5	31	6	I47763	I47763 Sequence 35
C 40	11	35.5	35	6	AX181212	AX181212 Sequence
C 41	11	35.5	40	6	AR053660	AR053660 Sequence
C 42	11	35.5	40	6	AR053705	AR053705 Sequence
C 43	11	35.5	40	6	AR054939	AR054939 Sequence
C 44	11	35.5	40	6	AR093969	AR093969 Sequence
C 45	11	35.5	40	6	AR175941	AR175941 Sequence

ALIGNMENTS

RESULT 1	AR016054/c	AR016054	30 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	Sequence 22 from patent US 5776679.					
DEFINITION	Sequence 22 from patent US 5776679.					
ACCESSION	AR016054					
VERSION	AR016054.1	GI:3972331				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 30)					
AUTHORS	Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.					
TITLE	Assays for the DNA component of human telomerase					
JOURNAL	Patent: US 5776679-A 22 07-JUL-1998;					
FEATURES	Location/Qualifiers					

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BASE COUNT 13 a 6 c 11 g 0 t
ORIGIN
Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 2
AR059215/c
LOCUS AR059215 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5837857.
ACCESSION AR059215
VERSION AR059215.1 GI:5984792
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 22 17-NOV-1998;
FEATURES
Location/Qualifiers
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Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 3
AR075526/c
LOCUS AR075526 30 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 23 from patent US 5958680.
ACCESSION AR075526
VERSION AR075526.1 GI:10002274
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 23 28-SEP-1999;
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 4
AR059215/c
LOCUS AR059215 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5837857.
ACCESSION AR059215
VERSION AR059215.1 GI:5984792
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 22 17-NOV-1998;
FEATURES
Location/Qualifiers
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BASE COUNT 13 a 6 c 11 g 0 t
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Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 5
I31769/c
LOCUS I31769 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 22 from patent US 5583016.
ACCESSION I31769
VERSION I31769.1 GI:1822560
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5583016-A 22 10-DEC-1996;
FEATURES
Location/Qualifiers
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BASE COUNT 13 a 6 c 11 g 0 t
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Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGCTGTTTCTC 22
Db 22 CTCCTCCGCGCGCTGTTTCTC 1

RESULT 6
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LOCUS AR016060 28 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 28 from patent US 5776679.
ACCESSION AR016060
VERSION AR016060.1 GI:3972337
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 28 07-JUL-1998;
FEATURES
Location/Qualifiers
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source
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BASE COUNT      12 a      6 c      10 g      0 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.086; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 7
LOCUS      AR075532/c
DEFINITION Sequence 29 from patent US 5958680.
ACCESSION  AR075532
VERSION     AR075532.1 GI:10002280
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE       Mammalian telomerase
JOURNAL     Patent: US 5958680-A 29 28-SEP-1999;
FEATURES    Location/Qualifiers
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BASE COUNT   12 a      6 c      10 g      0 t
ORIGIN

Query Match      67.7%; Score 21; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.086; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 CTCCTCCGCGCGCTGTTTCT 21
Db 21 CTCCTCCGCGCGCTGTTTCT 1

RESULT 8
LOCUS      AX019577/c
DEFINITION Sequence 31 from Patent WO9938964.
ACCESSION  AX019577
VERSION     AX019577.1 GI:10043491
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Keith,W.N.
TITLE       Promoter regions of the mouse and human telomerase rna component
JOURNAL     Patent: WO 9938964-A 31 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES    Location/Qualifiers
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BASE COUNT   6 a      5 c      7 g      2 t
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Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TTCTCGCTGACTT 30
Db 20 TTCTCGCTGACTT 8

RESULT 9
LOCUS      AX019580/c
DEFINITION Sequence 34 from Patent WO9938964.
ACCESSION  AX019580
VERSION     AX019580.1 GI:10043494
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Keith,W.N.
TITLE       Promoter regions of the mouse and human telomerase rna component
JOURNAL     Patent: WO 9938964-A 34 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES    Location/Qualifiers
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Query Match      41.9%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TTCTCGCTGACTT 30
Db 20 TTCTCGCTGACTT 8

RESULT 10
LOCUS      AX019578/c
DEFINITION Sequence 32 from Patent WO9938964.
ACCESSION  AX019578
VERSION     AX019578.1 GI:10043492
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Keith,W.N.
TITLE       Promoter regions of the mouse and human telomerase rna component
JOURNAL     Patent: WO 9938964-A 32 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES    Location/Qualifiers
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Query Match      41.9%; Score 13; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TTCTCGCTGACTT 30
Db 29 TTCTCGCTGACTT 17

RESULT 11
LOCUS      AR076656/c
DEFINITION Sequence 21 from patent US 5959096.
ACCESSION  AR076656
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VERSION AR076656.1 GI:10003402
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5959096-A 21 28-SEP-1999;
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BASE COUNT 2 a 7 c 8 g 3 t
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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
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Db 18 CTCCTCCGCGCGC 7

RESULT 12
LOCUS AR076657/c
DEFINITION Sequence 22 from patent US 5959096.
ACCESSION AR076657
VERSION AR076657.1 GI:10003403
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5959096-A 22 28-SEP-1999;
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BASE COUNT 2 a 6 c 11 g 1 t
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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
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Db 18 CTCCTCCGCGCGC 7

RESULT 13
LOCUS AR182713/c
DEFINITION Sequence 21 from patent US 6339066.
ACCESSION AR182713
VERSION AR182713.1 GI:20225920
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of high chiral purity and which modulate .beta.I., .beta.II., .gamma., .delta., .EPSILON., .zeta. and .eta. isoforms of human protein kinase C
JOURNAL Patent: US 6339066-A 21 15-JAN-2002;
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BASE COUNT 2 a 7 c 8 g 3 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
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Db 13 CTCCTCCGCGCGC 2

RESULT 14
LOCUS AR182714/c
DEFINITION Sequence 22 from patent US 6339066.
ACCESSION AR182714
VERSION AR182714.1 GI:20225921
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of high chiral purity and which modulate .beta.I., .beta.II., .gamma., .delta., .EPSILON., .zeta. and .eta. isoforms of human protein kinase C
JOURNAL Patent: US 6339066-A 22 15-JAN-2002;
FEATURES
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BASE COUNT 2 a 6 c 11 g 1 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 13 CTCCTCCGCGCGC 2

RESULT 15
LOCUS AX226311/c
DEFINITION Sequence 21 from Patent EP1126025.
ACCESSION AX226311
VERSION AX226311.1 GI:15555575
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Dean,N.
TITLE Oligonucleotide modulation of protein kinase c
JOURNAL Patent: EP 1126025-A 21 22-AUG-2001;
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    /db_xref="taxon:32630"
    /note="Artificial"
BASE COUNT 2 a 7 c 8 g 3 t
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCGCGC 12
    |||||
Db 13 CTCCTCCGCGCGC 12
```

RESULT 9
 AZ332622/c
 LOCUS
 DEFINITION
 35 bp DNA linear GSS 29-SEP-2000
 1M0061M11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0061M11 P, DNA sequence.

ACCESSION
 AZ332622
 VERSION
 AZ332622.1 GI:10396450
 KEYWORDS
 GSS.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 35)

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 UNPUBLISHED (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 5607
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0061 row: M column: 11
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 35.

FEATURES

source

1..35
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0061M11"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI14732114|95|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

ORIGIN

9 a 5 c 11 g 10 t

Query Match 36.7%; Score 11; DB 17; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCCATTTTTT 19

|||||

15 GGCCATTTTTT 5

Db

RESULT 10

AL764814/c
 LOCUS

DEFINITION
 Arabidopsis thaliana T-DNA flanking sequence GK-131C11-012721,
 genomic survey sequence.

ACCESSION
 AL764814
 VERSION
 AL764814.1 GI:21517857
 KEYWORDS
 GSS.
 SOURCE
 thale cress.

ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
 AUTHORS
 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
 and Weisshaar, B.

TITLE
 A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines

JOURNAL
 UNPUBLISHED
 COMMENT
 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics

UNPUBLISHED
 3 (bases 1 to 40)
 Li, Y., Rosso, M., Strizhov, N. and Weisshaar, B.
 Direct Submission
 Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone MF020. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

1..40
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-131C11-012721"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA from
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT 15 a 5 c 11 g 8 t 1 others

ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATTTTGTGCT 23

|||||

21 ATTTTGTGCT 11

Db

RESULT 11

AI266869
 LOCUS

DEFINITION
 IMAGE:1891290 3' similar to SW:ATP6_MOUSE P00848 ATP SYNTHASE A
 CHAIN;; mRNA sequence.

ACCESSION
 AI266869
 VERSION
 AI266869.1 GI:3885027

AI266869
 uJ08a10.x1 Sugano mouse liver mlta Mus musculus cDNA clone

43 bp mRNA linear EST 16-NOV-1998

Db 18 CTCCTCCGCGCGC 7

Search completed: June 23, 2003, 20:29:43
Job time : 310.975 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:08:34 ; Search time 785.207 Seconds
(without alignments)
618.773 Million cell updates/sec

Title: US-08-770-564A-1_COPY_290_319

Perfect score: 30

Sequence: 1 GGGGTGGTGGCCATTTTGTCTAACCCCTA 30

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfum:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	46.7	42	10 AV832474	AV832474 AV832474
C 2	13	43.3	37	9 AI862676	AI862676 wj27f04.x
C 3	11	36.7	19	17 A2514722	A2514722 IM0361C10
C 4	11	36.7	30	2 HSM001897	AI037566 Homo sapi
C 5	11	36.7	31	9 AI189788	AI189788 qc33c03.x
C 6	11	36.7	33	17 AL756125	AL756125 Arabidops

C 7	11	36.7	34	9 AA911862	AA911862 OG21a09.s
C 8	11	36.7	34	9 AI623585	AI623585 t837f06.x
C 9	11	36.7	35	17 AZ332622	AZ332622 IM0061M11
C 10	11	36.7	40	17 AL764814	AL764814 Arabidops
C 11	11	36.7	43	9 AI266869	AI266869 wj08a10.x
C 12	11	36.7	45	17 BH813805	BH813805 SALK_0853
C 13	11	36.7	46	9 AI680115	AI680115 tw65a03.x
C 14	11	36.7	46	17 AZ404140	AZ404140 IM0172J15
C 15	11	36.7	50	9 AI105989	AI105989 AU105989
C 16	11	36.7	50	9 AA257872	AA257872 MBL2S34F5
C 17	10	33.3	18	17 AZ294200	AZ294200 4905.ic27
C 18	10	33.3	19	9 AA909236	AA909236 ol08a11.s
C 19	10	33.3	23	17 AZ329120	AZ329120 IM0053A14
C 20	10	33.3	23	17 AZ481914	AZ481914 IM0306K03
C 21	10	33.3	24	17 AZ333171	AZ333171 IM0062B08
C 22	10	33.3	25	9 AA912548	AA912548 ol36c01.s
C 23	10	33.3	25	9 AL048782	AL048782 DKFZP5660
C 24	10	33.3	25	17 AZ873581	AZ873581 ZM0187G19
C 25	10	33.3	26	10 AW698828	AW698828 r435 non-
C 26	10	33.3	28	9 AI377008	AI377008 tc34h10.x
C 27	10	33.3	28	9 AI635476	AI635476 t865a03.x
C 28	10	33.3	28	17 AZ456389	AZ456389 IM0259B23
C 29	10	33.3	28	17 AZ591734	AZ591734 IM0402D05
C 30	10	33.3	28	17 AZ640640	AZ640640 IM0502H13
C 31	10	33.3	29	17 AZ308439	AZ308439 IM0011I20
C 32	10	33.3	29	17 AZ800642	AZ800642 ZM0058G16
C 33	10	33.3	31	2 HSM003598	AI039122 Homo sapi
C 34	10	33.3	31	9 AI004906	AI004906 ou59e11.x
C 35	10	33.3	31	9 AI200650	AI200650 qf94a11.x
C 36	10	33.3	31	9 AI364767	AI364767 qm18d02.x
C 37	10	33.3	31	17 AZ464939	AZ464939 IM0274I06
C 38	10	33.3	32	10 AV962684	AV962684 AV962684
C 39	10	33.3	32	17 AZ471070	AZ471070 IM0285A02
C 40	10	33.3	32	17 DR9H23S	AL743393 Danio rer
C 41	10	33.3	34	9 AA861409	AA861409 ak34a12.s
C 42	10	33.3	34	9 AI149355	AI149355 qc82b03.x
C 43	10	33.3	34	9 AU013748	AU013748 AU013748
C 44	10	33.3	34	9 AU256767	AU256767 AU256767
C 45	10	33.3	34	13 BJ077096	BJ077096 BJ077096

ALIGNMENTS

RESULT 1
AV832474/c
LOCUS AV832474 42 bp mRNA linear EST 22-JUN-2001
DEFINITION AV832474 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA clone baak3h01, mRNA sequence.
ACCESSION AV832474.1 GI:14524563
VERSION EST.
KEYWORDS Hordeum vulgare subsp. vulgare.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 42)
Sato, K.
AUTHORS Barley EST sequencing project in NIG and Okayama Univ
TITLE Unpublished (2001)
JOURNAL Contact: Kazuhiro Sato
COMMENT Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kzsato@rib.okayama-u.ac.jp,
URL: http://www.rib.okayama-u.ac.jp/barley/
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct
submission;
database: http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
1. 42

FEATURES

source

```

/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref="taxon:112503"
/clone="baak3h01"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
/tissue_type="leaves"
/dev_stage="vegetative stage"
16 a 6 c 5 g 14 t 1 others
BASE COUNT
ORIGIN

Query Match 46.7%; Score 14; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CATTCTTTGTCTAA 25
Db 35 CATTCTTTGTCTAA 22

RESULT 2
AI862676
LOCUS
DEFINITION
AI862676 37 bp mRNA linear EST 21-DEC-1999
similar to SW:TENS_CHICK Q04205 TENSIN.1, mRNA sequence.
ACCESSION
AI862676 1 GI:5526783
VERSION
AI862676
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 970 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Features
Location/Qualifiers
1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2404063"
/clone_lib="NCI CGAP Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."
4 a 14 c 15 g 4 t
BASE COUNT
ORIGIN

/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref="taxon:112503"
/clone="baak3h01"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
/tissue_type="leaves"
/dev_stage="vegetative stage"
16 a 6 c 5 g 14 t 1 others
BASE COUNT
ORIGIN

Query Match 43.3%; Score 13; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGCCA 13
Db 24 GGGGTGGTGGCCA 36

RESULT 3
AZ514722
LOCUS
DEFINITION
IM0361C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0361C10 R, DNA sequence.
ACCESSION
AZ514722
VERSION
AZ514722.1 GI:10696038
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: C column: 10
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Features
Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361C10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
3 a 4 c 4 g 8 t
BASE COUNT
ORIGIN

```

```

Query Match      36.7%; Score 11; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGCCATTTT 18
DB 7 TGGCCATTTT 17

RESULT 4
HSM001897/c
ID HSM001897 standard; RNA; EST; 30 BP.
XX AL037566;
XX AL037566.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZP564I1472_r1 (from clone DKFZP564I1472)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RP 1-30
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source
FH 1..30
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone="DKFZP564I1472"
FH /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FH X1-2blue; sites NotI + SalI"
FH /dev_stage="fetal"
FH /tissue_type="brain"
XX
SQ Sequence 30 BP; 22 A; 2 C; 4 G; 1 T; 1 other;

Query Match      36.7%; Score 11; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTTTGTCTA 24
DB 18 TTTTGTCTA 8

RESULT 5
AI189788/c
LOCUS AI189788 31 bp mRNA linear EST 28-OCT-1998
DEFINITION g333403.x1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA
clone IMAGE:1725509 3' similar to SW:PRP2 HUMAN P02812 SALIVARY
PROLINE-RICH PROTEIN PRECURSOR ; contains element TAR1 repetitive
element ;, mRNA sequence.
ACCESSION AI189788
VERSION AI189788.1 GI:3740997

```

```

KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE 1 (bases 1 to 31)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 977 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..31
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1725509"
/clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCCGCGATTTTTTTITTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 12 a 12 c 6 g 1 t
ORIGIN
Query Match      36.7%; Score 11; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCCATTTT 19
DB 14 GGCCATTTT 4

RESULT 6
AL756125
LOCUS AL756125.1 GI:21488623
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-105G12-012137,
genomic survey sequence.
ACCESSION AL756125
VERSION AL756125.1 GI:21488623
KEYWORDS GSS.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
thale cress.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weissehaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissehaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
JOURNAL

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 23, 2003, 01:05:28 ; Search time 348.884 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-8
Perfect score: 30
Sequence: 1 GCTTAGAATGAACGGTGGAGGGCGGAGG 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

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28: em_un.*

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30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

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34: em_htg_pln.*

35: em_htg_rod.*

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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	100.0	30	6	AX465471 Sequence
3	29	96.7	30	6	A84596 Sequence
4	29	96.7	30	6	AR079893 Sequence
5	23	76.7	27	6	AR063850 Sequence
6	23	76.7	27	6	AX317989 Sequence
7	22	73.3	26	6	A94988 Sequence
8	22	73.3	26	6	AR016055 Sequence
9	22	73.3	26	6	AR028786 Sequence
10	22	73.3	26	6	AR059216 Sequence
11	22	73.3	26	6	AR075527 Sequence
12	22	73.3	26	6	AR161925 Sequence
13	22	73.3	26	6	AX022187 Sequence
14	22	73.3	26	6	AX033377 Sequence
15	22	73.3	26	6	AX468455 Sequence
16	22	73.3	26	6	BD011297 Human tel
17	22	73.3	26	6	E36508 Method for
18	22	73.3	26	6	E37046 Human telom
19	22	73.3	26	6	I31770 Sequence 23
20	19	63.3	19	6	AR063833 Sequence
21	15	50.0	15	6	AR063834 Sequence
22	13	43.3	18	6	BD011244 Human tel
23	13	43.3	18	6	E36993 Sequence
24	13	43.3	28	6	AX298137 Sequence
25	13	43.3	46	6	AX212280 Sequence
26	12	40.0	17	6	AX099957 Sequence
27	12	40.0	24	6	AX196969 Sequence
28	12	40.0	24	6	AX446688 Sequence
29	12	40.0	25	6	I04124 Sequence 8
30	12	40.0	26	6	AR000025 Sequence
31	12	40.0	26	6	AR169136 Sequence
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33	12	40.0	26	6	AX036237 Sequence
34	12	40.0	30	6	AR142056 Sequence
35	12	40.0	30	6	I25474 Sequence 3
36	12	40.0	30	6	I59923 Sequence 50
37	12	40.0	30	6	I86781 Sequence 50
38	12	40.0	30	6	I95806 Sequence 50
39	12	40.0	34	6	E47160 Method for
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41	12	40.0	39	6	E49124 Novel G pro
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43	11	36.7	11	6	AR063835 Sequence
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ALIGNMENTS

RESULT 1
AR063832
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR063832
Sequence 8 from patent US 5846723.
AR063832
AR063832.1 GI:5993140
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 30)
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 8 08-DEC-1998;
Location/Qualifiers

30 bp
DNA
linear
PAT 29-SEP-1999

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DEFINITION Sequence 2 from Patent WO204681.
ACCESSION  AX465471
VERSION     AX465471.1 GI:21899833
KEYWORDS   synthetic construct.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Letsinger,R.L. and Garimella,V.
TITLE      Method of detection by enhancement of silver staining
JOURNAL    Patent: WO 0204681-A 2 17-JAN-2002;
NORTHWESTERN UNIVERSITY (US)
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 6 from Patent WO9845450.
ACCESSION  A84596
VERSION     A84596.1 GI:6733512
KEYWORDS   unidentified.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Atkinson,E.M. and Kealey,J.T.
TITLE      PURIFIED TELOMERASE
JOURNAL    Patent: WO 9845450-A 6 15-OCT-1998;
GERON CORP (US)
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DEFINITION Sequence 6 from patent US 5968506.
ACCESSION  AR079893
VERSION     AR079893.1 GI:10006646
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Weinrich,S.L., Atkinson,E.M. III, Lichtesteiner,S.P., Vasserot,A.P.,
            Pruzan,R.A. and Kealey,J.T.
TITLE      Purified telomerase
JOURNAL    Patent: US 5968506-A 6 19-OCT-1999;
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Db 2 CTCTAGATGAACGGTGAAGCGGCAGG 30

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DEFINITION Sequence 26 from patent US 5846723.
ACCESSION  AR063850
VERSION     AR063850.1 GI:5993158
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 27)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 26 08-DEC-1998;
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RESULT 6
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DEFINITION Sequence 2 from Patent WO0190409.
ACCESSION  AX317989
VERSION     AX317989.1 GI:17900798
KEYWORDS   
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DEFINITION		Sequence 26 from patent US 5858777.					
ACCESSION		AR028786					
VERSION		AR028786.1 GI:5940759					
KEYWORDS		Unknown.					
SOURCE		Unknown.					
ORGANISM		Unclassified.					
REFERENCE		1. (bases 1 to 26)					
AUTHORS		Villéponteau, B., Feng, J., Andrews, W.H. and Adams, R.R.					
TITLE		Methods and reagents for regulating telomere length and telomerase activity					
JOURNAL		Patent: US 5858777-A 26 12-JAN-1999;					
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ACCESSION		AR059216					
VERSION		AR059216.1 GI:5984793					
KEYWORDS		Unknown.					
SOURCE		Unknown.					
ORGANISM		Unclassified.					
REFERENCE		1. (bases 1 to 26)					
AUTHORS		Villéponteau, B., Feng, J., Funk, W. and Andrews, W.H.					
TITLE		Mammalian telomerase					
JOURNAL		Patent: US 5837857-A 23 17-NOV-1998;					
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LOCUS AR075527 26 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5958680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 24 28-SEP-1999;
FEATURES Location/Qualifiers
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RESULT 12
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DEFINITION Sequence 23 from patent US 6258535.
ACCESSION AR161925
VERSION AR161925.1 GI:16228953
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 23 10-JUL-2001;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 3 c 9 g 7 t
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
LOCUS AX022187 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent EP0953042.
ACCESSION AX022187
VERSION AX022187.1 GI:10045855
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Andrews,W.H., Villeponteau,B., Adams,R.R. and Feng,J.
TITLE Methods and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: EP 0953042-A 26 03-NOV-1999;
FEATURES GERON CORP (US) Location/Qualifiers

Query Match 73.3%; Score 22; DB 6; Length 26;
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RESULT 14
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DEFINITION Sequence 9 from Patent WO0046601.
ACCESSION AX033377
VERSION AX033377.1 GI:10280151
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 9 10-AUG-2000;
FEATURES LARSEN FRANK (NO); SKAANSENG MARIANNE (NO) Location/Qualifiers
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DEFINITION Sequence 5 from Patent WO0218652.
ACCESSION AX468455
VERSION AX468455.1 GI:21901291
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Koprski,M.S. and Gocke,C.D.
TITLE Method for detection of htr and htert telomerase-associated rna in plasma or serum
JOURNAL Patent: WO 0218652-A 5 07-MAR-2002;
FEATURES Oncomedx, Inc. (US) Location/Qualifiers
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DEFINITION Sequence 5 from Patent WO0218652.
ACCESSION AX468455
VERSION AX468455.1 GI:21901291
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Koprski,M.S. and Gocke,C.D.
TITLE Method for detection of htr and htert telomerase-associated rna in plasma or serum
JOURNAL Patent: WO 0218652-A 5 07-MAR-2002;
FEATURES Oncomedx, Inc. (US) Location/Qualifiers
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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31	11	36.7	22	10	US-09-785-873A-5	Sequence 5, Appl
32	11	36.7	23	9	US-09-952-522B-9	Sequence 2, Appl
33	11	36.7	24	9	US-10-245-813-2	Sequence 1005, Ap
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42	11	36.7	25	9	US-10-098-263B-104702	Sequence 117265, A
43	11	36.7	25	9	US-10-098-263B-117265	Sequence 5488, Ap
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ALIGNMENTS

RESULT 1
US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGAACGGTGGAG 22
Db 5 GCTCTAGAATGAACGGTGGAG 26

RESULT 2
US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGAACGGTGGAG 22
Db 5 GCTCTAGAATGAACGGTGGAG 26

RESULT 3
US-09-057-351-23
Sequence 23, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match      73.3%; Score 22; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGAAG 22
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Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 4
US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118949

Query Match      43.3%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATGAACG 15
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Db 20 TCTAGAAATGAACG 8

RESULT 5
US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 3048.770811
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer

US-09-952-522B-19
Query Match      43.3%; Score 13; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
   |||||
Db 1 GCTCTAGAAATGAA 13

RESULT 6
US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match      43.3%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
   |||||
Db 1 GCTCTAGAAATGAA 13

RESULT 7
US-09-780-566-11/c
; Sequence 11, Application US/09780566
; Patent No. US20020111289A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Herweking, Heiko
; TITLE OF INVENTION: CDK4 IS A TARGET OF C-MYC
; FILE REFERENCE: 01107.00092
; CURRENT APPLICATION NUMBER: US/09/780,566
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,930
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primers
US-09-780-566-11

Query Match      43.3%; Score 13; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 GGTGAAGCGGC 27
 Db 24 GGTGAAGCGGC 12

RESULT 8
 US-09-969-373-1959
 ; Sequence 1959, Application US/09969373
 ; Patent No. US2002013852A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Effertz, Roger J.
 ; APPLICANT: Hauge, Brian M.
 ; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
 ; FILE REFERENCE: 38-10(52679)A
 ; CURRENT APPLICATION NUMBER: US/09/969,373
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 09/754,853
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: US 09/760,427
 ; PRIOR FILING DATE: 2001-01-13
 ; PRIOR APPLICATION NUMBER: US 09/855,768
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 4593
 ; SEQ ID NO 1959
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-969-373-1959

Query Match 40.0%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATGAACGGTGG 20
 Db 6 ATGAACGGTGG 17

RESULT 9
 US-09-952-522B-17
 ; Sequence 17, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benhaim, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; APPLICANT: Zhu, Min
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448.77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/06232
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 60/123,711
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/162,462
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
 OTHER INFORMATION: forward primer

US-09-952-522B-17

Query Match 40.0%; Score 12; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAATGA 12
 Db 1 GCTCTAGAATGA 12

RESULT 10
 US-09-952-522B-31
 ; Sequence 31, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benhaim, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; APPLICANT: Zhu, Min
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448.77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/06232
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 60/123,711
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/162,462
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
 OTHER INFORMATION: forward primer
 US-09-952-522B-31

Query Match 40.0%; Score 12; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGA 12
 Db 1 GCTCTAGAATGA 12

RESULT 11
 US-09-754-853A-676
 ; Sequence 676, Application US/09754853A
 ; Publication No. US20030005491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hauge, Brian M.
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Parsons, Jeremy D.
 ; APPLICANT: Wang, Ming Li
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
 ; FILE REFERENCE: 38-10(15810)B
 ; FILE REFERENCE: 38-10(15810)B
 ; CURRENT APPLICATION NUMBER: US/09/754,853A
 ; CURRENT FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: US 60/174,880
 ; PRIOR FILING DATE: 2000-01-07
 ; NUMBER OF SEQ ID NOS: 1119
 ; SEQ ID NO 676
 ; LENGTH: 24
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 FEATURE:

OTHER INFORMATION: Clone ID: 318013_region_A3_187577_13_Reverse_Primer_Seq
US-09-754-853A-676

Query Match 40.0%; Score 12; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 ATGAACGGTGGG 20
DB 13 ATGAACGGTGGG 24

RESULT 12
US-09-940-185-3143/c
Sequence 3143, Application US/09940185
Publication No. US20030096239A1
GENERAL INFORMATION:
APPLICANT: Gunderson, Kevin
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3143
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-3143

Query Match 40.0%; Score 12; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 ACGGTGGAGGC 24
DB 16 ACGGTGGAGGC 5

RESULT 13
US-10-215-112-6862/c
Sequence 6862, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6862
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6862

Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGA 12

Db

15 GCTCTAGATGA 4

RESULT 14
US-10-215-112-8975
Sequence 8975, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8975
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8975

Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGGTGGAG 22
DB 5 GAACGGTGGAG 16

RESULT 15
US-10-215-112-13825/c
Sequence 13825, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13825
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-13825

Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGGTGGAG 22
DB 21 GAACGGTGGAG 10

Search completed: June 23, 2003, 20:01:32
Job time : 242.076 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 2516.18 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30

Sequence: 1 GCTCTAGATGAACGGTGAAGCGGCGAGG 30

Scoring table:

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Searched: 24791104 seqs, 12571243825 residues

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Minimum DB seq length: 0

Maximum DB seq length: 50

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- 43: /cgn2_6/ptodata/2/pna/US102B COMB.seq.*

- 44: /cgn2_6/ptodata/2/pna/US6000 COMB.seq.*
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- 46: /cgn2_6/ptodata/2/pna/US6002 COMB.seq.*
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- 48: /cgn2_6/ptodata/2/pna/US6004 COMB.seq.*
- 49: /cgn2_6/ptodata/2/pna/US6005 COMB.seq.*
- 50: /cgn2_6/ptodata/2/pna/US6006 COMB.seq.*
- 51: /cgn2_6/ptodata/2/pna/US6007 COMB.seq.*
- 52: /cgn2_6/ptodata/2/pna/US6008 COMB.seq.*
- 53: /cgn2_6/ptodata/2/pna/US6009 COMB.seq.*
- 54: /cgn2_6/ptodata/2/pna/US6010 COMB.seq.*
- 55: /cgn2_6/ptodata/2/pna/US6011 COMB.seq.*
- 56: /cgn2_6/ptodata/2/pna/US6012 COMB.seq.*
- 57: /cgn2_6/ptodata/2/pna/US6013 COMB.seq.*
- 58: /cgn2_6/ptodata/2/pna/US6014 COMB.seq.*
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- 65: /cgn2_6/ptodata/2/pna/US6021 COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6022 COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6023 COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6024 COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6025 COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6026 COMB.seq.*
- 71: /cgn2_6/ptodata/2/pna/US6027 COMB.seq.*
- 72: /cgn2_6/ptodata/2/pna/US6028 COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6029 COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6030 COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6031 COMB.seq.*
- 76: /cgn2_6/ptodata/2/pna/US6032 COMB.seq.*
- 77: /cgn2_6/ptodata/2/pna/US6033 COMB.seq.*
- 78: /cgn2_6/ptodata/2/pna/US6034 COMB.seq.*
- 79: /cgn2_6/ptodata/2/pna/US6035 COMB.seq.*
- 80: /cgn2_6/ptodata/2/pna/US6036 COMB.seq.*
- 81: /cgn2_6/ptodata/2/pna/US6037 COMB.seq.*
- 82: /cgn2_6/ptodata/2/pna/US6038 COMB.seq.*
- 83: /cgn2_6/ptodata/2/pna/US6039 COMB.seq.*
- 84: /cgn2_6/ptodata/2/pna/US6040 COMB.seq.*
- 85: /cgn2_6/ptodata/2/pna/US6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	30	1	PCT-US97-23619-8
2	30	100.0	30	9	US-08-510-736-5
3	30	100.0	30	11	US-08-770-564A-8
4	30	100.0	30	21	US-09-540-119B-10
5	30	100.0	30	28	US-09-717-828A-5
6	30	100.0	30	28	US-09-717-828B-5
7	30	100.0	30	28	US-09-717-829A-5
8	30	100.0	30	34	US-09-903-461-2
9	23	76.7	27	1	PCT-US97-23619-26
10	22	73.3	25	16	US-09-250-336A-4
11	22	73.3	25	25	US-09-642-177-4
12	22	73.3	26	1	PCT-US96-14679-27
13	22	73.3	26	1	PCT-US96-14679A-27
14	22	73.3	26	1	PCT-US99-03302-4
15	22	73.3	26	1	PCT-US99-07533-4
16	22	73.3	26	1	PCT-US99-07533-4
17	22	73.3	26	6	US-08-272-102-23
18	22	73.3	26	7	US-08-387-524-19
19	22	73.3	26	8	US-08-472-802A-24
20	22	73.3	26	8	US-08-472-802B-24
21	22	73.3	26	8	US-08-482-115A-23

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22 22 73.3 26 9 US-08-520-550-19
23 22 73.3 26 9 US-08-521-634-41
24 22 73.3 26 10 US-08-660-678-23
25 22 73.3 26 13 US-08-911-312-23
26 22 73.3 26 13 US-08-911-312-23
27 22 73.3 26 13 US-08-911-312A-23
28 22 73.3 26 13 US-08-912-951-312
29 22 73.3 26 13 US-08-973-589-17
30 22 73.3 26 13 US-08-974-549-598
31 22 73.3 26 14 US-09-057-351-23
32 22 73.3 26 16 US-09-216-847-2
33 22 73.3 26 16 US-09-250-336-4
34 22 73.3 26 16 US-09-259-943-45
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36 22 73.3 26 18 US-09-402-181B-598
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38 22 73.3 26 25 US-09-653-573-5
39 22 73.3 26 29 US-09-721-477-598
40 22 73.3 26 29 US-09-721-506-598
41 22 73.3 26 33 US-09-890-567-9
42 22 73.3 26 33 US-09-895-606-26
43 22 73.3 26 38 US-10-044-539-312
44 22 73.3 26 38 US-10-044-692-312
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19 63.3 19 11 US-08-770-564A-9

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ALIGNMENTS

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RESULT 1
PCT-US97-23619-8
; Sequence 8, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..30
; OTHER INFORMATION: /note="oligo 21"
PCT-US97-23619-8

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTAGAATGAACGGTGGAGCGGCAGG 30
Db 1 GCTTAGAATGAACGGTGGAGCGGCAGG 30

RESULT 2
US-08-510-736-5
; Sequence 5, Application US/08510736
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Methods for Purifying Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,736
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 015389-001100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-510-736-5

Query Match 100.0%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTAGAATGAACGGTGGAGCGGCAGG 30
Db 1 GCTTAGAATGAACGGTGGAGCGGCAGG 30

RESULT 3

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US-08-770-564A-8
; Sequence 8, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-8

Query Match 100.0%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30
DB 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30

RESULT 4
US-09-540-119B-10
; Sequence 10, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-10

Query Match 100.0%; Score 30; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30
DB 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30

RESULT 5
US-09-717-828A-5
; Sequence 5, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-5

Query Match 100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30
DB 1 GCTCTAGATGAACGGTGAAGCGGCGCAGG 30

RESULT 6
US-09-717-828B-5
; Sequence 5, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828B-5

Query Match      100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 7
US-09-717-829A-5
; Sequence 5, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Allain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1 edited
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-5

Query Match      100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 8
US-09-903-461-2
; Sequence 2, Application US/09903461
; GENERAL INFORMATION:
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Garimella, Viswanadham
; TITLE OF INVENTION: Method of Detection by Enhancement of Silver Staining
; FILE REFERENCE: 00-1086-A
; CURRENT APPLICATION NUMBER: US/09/903,461
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/217,782
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 98
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-09-903-461-2

Query Match      100.0%; Score 30; DB 34; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
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Db 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 9
PCT-US97-23619-26
; Sequence 26, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..27
; OTHER INFORMATION: /note= "htr reverse primer"
PCT-US97-23619-26

Query Match      76.7%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGG 23
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Db 5 GCTCTAGTAATGAACGGTGAAGC 27
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RESULT 10
US-09-250-336A-4
; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT APPLICATION NUMBER: US/09/250,336A
; CURRENT FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 73.3%; Score 22; DB 16; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACGGTGAAG 22
|||||

Db 4 GCTCTAGTAATGAACGGTGAAG 25
|||||

RESULT 11
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 73.3%; Score 22; DB 25; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACGGTGAAG 22

Db 4 GCTCTAGTAATGAACGGTGAAG 25
|||||

RESULT 12
PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACGGTGAAG 22
|||||

Db 5 GCTCTAGTAATGAACGGTGAAG 26
|||||

RESULT 13
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.

ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/14679A
FILING DATE: 13-SEP-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KASTER ESQ., KEVIN R.
REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 012/045PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 473-7779
TELEFAX: (415) 473-7750
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGGAAG 22
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Db 5 GCTCTAGAAATGAACGGTGGGAAG 26

RESULT 14

PCT-US99-03302-4

; Sequence 4, Application PC/TUS9903302

; GENERAL INFORMATION:

; APPLICANT: Strovel, Jeffrey W

; APPLICANT: Stamberg, Judith

; APPLICANT: Abruzzo, Lynne V

; APPLICANT: Highsmith, Edward

; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening

; FILE REFERENCE: 1489US 60/074,793

; CURRENT APPLICATION NUMBER: PCT/US99/03302

; CURRENT FILING DATE: 1999-02-16

; EARLIER APPLICATION NUMBER: 60/074,793

; EARLIER FILING DATE: 1998-02-16

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 4

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: R3c,

; OTHER INFORMATION: synthesized, Gibco-BRL

PCT-US99-03302-4

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGGAAG 22
|||||
Db 5 GCTCTAGAAATGAACGGTGGGAAG 26

RESULT 15

PCT-US99-07533-4

; Sequence 4, Application PC/TUS9907533

; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157WO1
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGGAAG 22
|||||
Db 5 GCTCTAGAAATGAACGGTGGGAAG 26

Search completed: June 23, 2003, 16:08:21
Job time : 2517.25 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 1316.89 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-8
Perfect score: 30
Sequence: 1 GCTCTAGTAATGAACGGTGAAGCGGCAGG 30

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0
Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
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5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US03_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
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13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	10 US-10-330-872-5	Sequence 5, Appli
2	30	100.0	30	10 US-10-330-872A-5	Sequence 5, Appli
3	23	76.7	23	1 PCT-US03-04088-520	Sequence 520, App
4	22	73.3	23	1 PCT-US03-04088-529	Sequence 529, App
5	22	73.3	26	6 US-09-721-456-598	Sequence 598, App
6	22	73.3	26	9 US-10-325-810-598	Sequence 598, App
7	22	73.3	26	9 US-10-359-935-23	Sequence 23, Appl
8	21	70.0	21	1 PCT-US03-04088-587	Sequence 587, App
9	21	70.0	21	1 PCT-US03-04088-521	Sequence 521, App
10	20	66.7	21	1 PCT-US03-04088-592	Sequence 592, App
11	19	63.3	19	1 PCT-US03-04088-14	Sequence 14, Appl
12	19	63.3	19	1 PCT-US03-04088-257	Sequence 257, App
13	19	63.3	19	1 PCT-US03-04088-278	Sequence 278, App
14	19	63.3	21	1 PCT-US03-04088-538	Sequence 538, App
15	19	63.3	21	1 PCT-US03-04088-539	Sequence 539, App
16	19	63.3	21	1 PCT-US03-04088-542	Sequence 542, App
17	19	63.3	21	1 PCT-US03-04088-543	Sequence 543, App
18	19	63.3	21	1 PCT-US03-04088-546	Sequence 546, App
19	19	63.3	21	1 PCT-US03-04088-547	Sequence 547, App
20	19	63.3	21	1 PCT-US03-04088-550	Sequence 550, App

21	19	63.3	21	1	PCT-US03-04088-551	Sequence 551, App
c 22	19	63.3	21	1	PCT-US03-04088-554	Sequence 554, App
c 23	19	63.3	21	1	PCT-US03-04088-555	Sequence 555, App
24	19	63.3	21	1	PCT-US03-04088-558	Sequence 558, App
25	19	63.3	21	1	PCT-US03-04088-559	Sequence 559, App
c 26	14	46.7	23	9	US-10-310-188-36216	Sequence 36216, A
27	14	46.7	24	8	US-10-442-506-39	Sequence 39, Appl
28	14	46.7	25	12	US-60-427-808-952738	Sequence 952738, A
29	14	46.7	25	13	US-60-469-545-13722	Sequence 13722, A
c 30	14	46.7	25	13	US-60-469-545-222991	Sequence 222991, A
31	13	43.3	18	6	US-09-721-456-543	Sequence 543, App
32	13	43.3	18	6	US-10-325-810-543	Sequence 543, App
c 33	13	43.3	25	6	US-09-660-222-3845	Sequence 3845, Ap
c 34	13	43.3	25	6	US-09-660-222-3846	Sequence 3846, Ap
c 35	13	43.3	25	6	US-09-660-222-3854	Sequence 3854, Ap
c 36	13	43.3	25	9	US-10-098-263B-118949	Sequence 118949, A
c 37	13	43.3	25	9	US-10-355-577-90268	Sequence 90268, A
c 38	13	43.3	25	9	US-10-355-577-173196	Sequence 173196, A
c 39	13	43.3	25	9	US-10-355-577-231533	Sequence 231533, A
40	13	43.3	25	9	US-10-355-577-579523	Sequence 579523, A
c 41	13	43.3	25	12	US-60-427-808-738286	Sequence 738286, A
c 42	13	43.3	25	12	US-60-427-808-843246	Sequence 843246, A
43	13	43.3	25	12	US-60-427-836-69383	Sequence 69383, A
44	13	43.3	25	12	US-60-427-836-267834	Sequence 267834, A
45	12	40.0	18	9	US-10-310-188-60169	Sequence 60169, A

ALIGNMENTS

RESULT 1
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.le-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACGGTGAAGCGGCAGG 30
Db 1 GCTCTAGTAATGAACGGTGAAGCGGCAGG 30

RESULT 2
US-10-330-872A-5
; Sequence 5, Application US/10330872A

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; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vassero, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-330-872A-5

Query Match      100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGAAGCGGCAGG 30

RESULT 3
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-529
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; OTHER INFORMATION: region
PCT-US03-04088-520

Query Match      76.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAGG 23
DB 23 GCTCTAGATGAACGGTGAAGG 1

RESULT 4
PCT-US03-04088-529/c
; Sequence 529, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-529

Query Match      73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGAAGCGGCAGG 30
DB 23 ATGAACGGTGAAGCGGCAGG 2

RESULT 5
US-09-721-456-598
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/721,456
  FILING DATE: 22-Nov-2000
  CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/974,549A
  FILING DATE: 19-Nov-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/911,312
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/912,951
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/915,503
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
  LENGTH: 26 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
  NAME/KEY: -
  LOCATION: 1..26
  OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-721-456-598
Query Match 73.3%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
DB 5 GCTCTAGATGAACGGTGAAG 26
|||||
RESULT 6
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:

```

```

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/325,810
  FILING DATE: 20-Dec-2002
  CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/402,181
  FILING DATE: 29-Sep-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/911,312
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/912,951
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/915,503
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Ausubelus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
  LENGTH: 26 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
  NAME/KEY: -
  LOCATION: 1..26
  OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598
Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
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Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 7

US-10-359-935-23

; Sequence 23, Application US/10359935

; GENERAL INFORMATION:

; APPLICANT: Villeponteau, Bryant

; Feng, Junli

; Funk, Walter

; Andrews, William H.

; TITLE OF INVENTION: Mammalian Telomerase

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/359,935

; FILING DATE: 07-Feb-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/057,351

; FILING DATE: 08-APR-1994

; APPLICATION NUMBER: US 08/272,102

; FILING DATE: 07-JUL-1994

; APPLICATION NUMBER: US 08/330,123

; FILING DATE: 27-OCT-1994

; APPLICATION NUMBER: US 08/472,802

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 015389-000821US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-359-935-23

Query Match 73.3%; Score 22; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0089;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGAAG 22

|||||

Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 8

PCT-US03-04088-587/c

; Sequence 587, Application PC/TUS0304088

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; Applicant: McSwiggen, James

; Applicant: Beigelman, Leonid

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)

; FILE REFERENCE: 02-708-A (400/080)

; CURRENT APPLICATION NUMBER: PCT/US03/04088

; CURRENT FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/396,600

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 587

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

; OTHER INFORMATION: region

PCT-US03-04088-587

Query Match 70.0%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.034;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATGAACGGTGAACGGCGCAG 29

|||||

Db 21 ATGAACGGTGAACGGCGCAG 1

RESULT 9

PCT-US03-04088-521/c

; Sequence 521, Application PC/TUS0304088

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; Applicant: McSwiggen, James

; Applicant: Beigelman, Leonid

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

; FILE REFERENCE: 02-708-A (400/080)

; CURRENT APPLICATION NUMBER: PCT/US03/04088

; CURRENT FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/396,600

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 521

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Artificial

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 70.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.034; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 GCTCTAGTAATGAACGGTGGAA 21
|||||
Db 21 GCTCTAGTAATGAACGGTGGAA 1

RESULT 10
PCT-US03-04088-592
; Sequence 592, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-592

Query Match 66.7%; Score 20; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 0.13; Mismatches 1; Indels 0; Gaps 0;
Matches 19; Conservative 1;

QY 11 GAACGGTGAACGGCGCAGG 30
|||||
Db 1 GAACGGUGGAGCGCGCAGG 20

RESULT 11
PCT-US03-04088-14/c
; Sequence 14, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088

; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-14

Query Match 63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 9 ATGAACGGTGAACGGCGC 27
|||||
Db 19 ATGAACGGTGAACGGCGC 1

RESULT 12
PCT-US03-04088-257/c
; Sequence 257, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 257
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-257

```
; OTHER INFORMATION: region
PCT-US03-04088-257

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GAACGGTGAAGCGGCAG 29
Db 19 GAACGGTGAAGCGGCAG 1

RESULT 13
PCT-US03-04088-278
; Sequence 278, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 0.49;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 9 ATGAACGGTGAAGCGGC 27
Db 1 AUGAACGGUGGAAGCGGC 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600

; OTHER INFORMATION: region
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TCTAGAATGAACGGTGGAA 21
Db 19 TCTAGAATGAACGGTGGAA 1

RESULT 15
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
PCT-US03-04088-538

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TCTAGAATGAACGGTGGAA 21
Db 19 TCTAGAATGAACGGTGGAA 1
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; OTHER INFORMATION: Description of Artificial Sequence:  s1NA sense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

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```

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGATGAACGGTGG 19
         |||||
Db      19 GCTCTAGATGAACGGTGG 1

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Job time : 1317.89 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1546.73 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30

Sequence: 1 GCTTAGAATGAACGGTGAAGGCGGAGG 30

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_nam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	40.0	37	9 A1358100	A1358100 qv96c06.x
C 2	11	36.7	37	9 AA388365	AA388365 vc94b10.r
C 3	11	36.7	38	9 AU256784	AU256784 AU256784
C 4	11	36.7	40	12 BF234348	BF234348 602026283
C 5	11	36.7	41	17 BH851717	BH851717 SALK 0734
C 6	11	36.7	48	17 AZ606694	AZ606694 1M0428D15

C 7	11	36.7	50	9 AUI04491	AUI04491 AUI04491
C 8	11	36.7	50	9 AUI04493	AUI04493 AUI04493
C 9	10	33.3	19	17 AZ471573	AZ471573 1M0286G13
C 10	10	33.3	28	17 TA116E03P	TA116E03P T. brucei
C 11	10	33.3	29	17 TA264G10Q	TA264G10Q T. brucei
C 12	10	33.3	31	9 AA912698	AA912698 ol30e02.s
C 13	10	33.3	31	17 TA106A06P	TA106A06P T. brucei
C 14	10	33.3	34	10 AV964763	AV964763 AV964763
C 15	10	33.3	34	14 T74961	T74961 yc85b03.r1
C 16	10	33.3	43	17 BH811442	BH811442 SALK 0586
C 17	10	33.3	46	9 AA681423	AA681423 vr41f08.s
C 18	10	33.3	46	13 BI822830	BI822830 603040148
C 19	10	33.3	49	17 AZ971265	AZ971265 2M0244N12
C 20	10	33.3	49	17 BH791685	BH791685 SALK 0608
C 21	10	33.3	50	9 AUI03954	AUI03954 AUI03954
C 22	10	33.3	50	9 AUI04288	AUI04288 AUI04288
C 23	10	33.3	50	9 AUI04289	AUI04289 AUI04289
C 24	10	33.3	50	9 AUI04290	AUI04290 AUI04290
C 25	10	33.3	50	9 AUI04291	AUI04291 AUI04291
C 26	10	33.3	50	9 AUI04292	AUI04292 AUI04292
C 27	10	33.3	50	9 AUI04294	AUI04294 AUI04294
C 28	10	33.3	50	9 AUI04295	AUI04295 AUI04295
C 29	10	33.3	50	9 AUI04299	AUI04299 AUI04299
C 30	10	33.3	50	9 AUI04305	AUI04305 AUI04305
C 31	10	33.3	50	9 AUI04306	AUI04306 AUI04306
C 32	10	33.3	50	9 AUI07444	AUI07444 AUI07444
C 33	10	33.3	50	9 AUI07670	AUI07670 AUI07670
C 34	10	33.3	50	9 AUI07671	AUI07671 AUI07671
C 35	10	33.3	50	9 AUI07673	AUI07673 AUI07673
C 36	10	33.3	50	9 AUI07674	AUI07674 AUI07674
C 37	10	33.3	50	9 AUI07679	AUI07679 AUI07679
C 38	10	33.3	50	9 AUI07681	AUI07681 AUI07681
C 39	10	33.3	50	9 AUI07682	AUI07682 AUI07682
C 40	10	33.3	50	9 AUI07683	AUI07683 AUI07683
C 41	10	33.3	50	9 AUI07930	AUI07930 AUI07930
C 42	10	33.3	50	9 AUI07932	AUI07932 AUI07932
C 43	10	33.3	50	17 AZ920773	AZ920773 1006022E0
C 44	9	30.0	22	9 AU259636	AU259636 AU259636
C 45	9	30.0	24	17 AZ662500	AZ662500 1M0541G07

ALIGNMENTS

RESULT 1
A1358100/c A1358100 37 bp mRNA linear EST 06-JAN-1999
LOCUS qv96c06.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:1989418 3
DEFINITION similar to SW:UIC6_HCMVA F16836 HYPOTHETICAL PROTEIN UL126. ; mRNA
sequence.
ACCESSION A1358100
VERSION A1358100 GI:4109721
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html


```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE          NIH-MGC http://mgc.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs@mail.nih.gov
               Tissue Procurement: Jeffrey E. Green, M.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: L1A9442 row: f column: 22
               High quality sequence stop: 40.
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                   /strain="FVB/N"
                   /db_xref="taxon:10090"
                   /clone_image="4161429"
                   /clone_lib="NCI_CGAP_L19"
                   /lab_host="DH10B (T1 phage-resistant)"
                   /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                   Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                   Average insert size 1.9 kb. Constructed by Life
                   Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT    3 a 12 c 13 g 12 t
ORIGIN
Query Match      36.7%; Score 11; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGAAGCGCGCA 28
Db      |||||
        29 GGAAGCGCGCA 19

RESULT 5
BH851717/c
LOCUS      BH851717
DEFINITION BH851717 41 bp DNA linear GSS 13-JUN-2002
           SALK_073411.49.55.x Arabidopsis thaliana TDNA insertion lines
           Arabidopsis thaliana genomic clone SALK_073411.49.55.x, DNA
           sequence.
ACCESSION  BH851717
VERSION     BH851717.1 GI:21422588
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana
           thale cress.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 41)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
           ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
           , Zimmerman,J. and Ecker,J.R.
           A Sequence-Indexed Library of Insertion Mutations in the
           Arabidopsis Genome
           Unpublished (2001)
           Contact: Joseph R. Ecker
           Salk Institute Genomic Analysis Laboratory (SIGNAL)
           The Salk Institute for Biological Studies
           10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
           Tel: 858 453 4100 x1752
           Fax: 858 558 6379
           Email: ecker@salk.edu
           This is single pass sequence recovered from the left border of
           TDNA.
           Class: TDNA tagged.

FEATURES      source
Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT    11 a 9 c 10 g 11 t
ORIGIN
Query Match      36.7%; Score 11; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 AACGGTGAAG 22
Db      |||||
        36 AACGGTGAAG 26

RESULT 6
AZ606694
LOCUS      AZ606694
DEFINITION 1M0428D15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
           clone UUGC1M0428D15 R, DNA sequence.
ACCESSION  AZ606694
VERSION     AZ606694.1 GI:11728884
KEYWORDS   GSS.
SOURCE     house mouse.
           Mus musculus
           Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 48)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
           Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
           ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
           and Wright,D., Weiss,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
           Unpublished (2000)
           Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: dunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0428 row: D column: 15
           Seq primer: CACACAGGAAACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 48.
           Location/Qualifiers
             1..48
               /organism="Mus musculus"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0428D15"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /sex="Male"
               /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA

```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 13 c 15 g 10 t

Query Match 36.7%; Score 11; DB 17; Length 48;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGACGGTGG 19
|||||

Db 38 ATGACGGTGG 48
|||||

RESULT 7
AUI04491/c
LOCUS
DEFINITION
AUI04491 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP22239, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
AUI04491.1 GI:13554012
EST.
human.

ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL
MEDLINE
COMMENT
EMBO Rep. 2 (5), 388-393 (2001)
21270072

Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP22239"

/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumurate treated U937 cells"

BASE COUNT 3 a 26 c 13 g 8 t

Query Match 36.7%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCGGCA 28
|||||

Db 28 GGAAGCGGCA 18
|||||

RESULT 8
AUI04493/c
LOCUS

DEFINITION
AUI04493 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADKA03063, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
AUI04493.1 GI:13554014
EST.
human.

ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL
MEDLINE
COMMENT
EMBO Rep. 2 (5), 388-393 (2001)
21270072

Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADKA03063"

/clone_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and
dimethylfumurate treated U937 cells"

BASE COUNT 4 a 26 c 13 g 7 t

Query Match 36.7%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGAAGCGGCA 28
|||||

Db 33 GGAAGCGGCA 23
|||||

RESULT 9
AZ471573/c
LOCUS

DEFINITION
AZ471573 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0286G13 F, DNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
AZ471573.1 GI:10629698
GSS.
house mouse.

ORGANISM
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 Row: G Column: 13
 Seq primer: CGTGTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UUGC1M0286G13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 3 c 6 g 4 t
 ORIGIN
 Query Match 33.3%; Score 10; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAATG 11
 |||||
 15 CTCTAGAATG 6

RESULT 10
 LOCUS
 DEFINITION
 T1.brucei sheared genomic DNA clone 116e03, forward sequence,
 genomic survey sequence.

ACCESSION
 AL462526
 VERSION
 AL462526.1 GI:11832364
 KEYWORDS
 GSS.
 SOURCE
 Trypanosoma brucei.
 ORGANISM
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 1 (bases 1 to 28)
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrall,B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrall, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 1. .29
 /organism="Trypanosoma brucei"
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 /clone="264G10"
 /clone="264G10"

BASE COUNT 11 a 5 c 11 g 2 t
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAATGAACG 15

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Db
|||||
7 AGATGAACG 16

RESULT 12
AA912698
LOCUS
DEFINITION
O130e02.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1524986 3' similar to TR:O14564 O14564 HYPOTHETICAL 67.1 KD
PROTEIN. 1, mRNA sequence.
AA912698
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 378 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..31
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CCGAP GCBI) were mixed, and ss circles were made in
viro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 8 a 7 c 12 g 4 t
ORIGIN
Query Match 33.3%; Score 10; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
21 AGCGGCAGG 30
|||||
14 AGCGGCAGG 23
Db

RESULT 13
TA106A06P
LOCUS
DEFINITION
TA106A06P 31 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 106a06, forward sequence,
Genomic survey sequence.
ACCESSION
AL459090
VERSION
AL459090.1 GI:11830967
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei.
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 31)
REFERENCE
"

AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
Location/Qualifiers
1..31
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="106a06"
BASE COUNT 8 a 11 c 7 g 5 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
11 GAACGGTGGG 20
|||||
13 GAACGGTGGG 22
Db

RESULT 14
AV964763/c
LOCUS
DEFINITION
AV964763 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad15006 5', mRNA sequence.
ACCESSION
AV964763
VERSION
AV964763.1 GI:19454459
KEYWORDS
EST.
SOURCE
Ciona intestinalis.
ORGANISM
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 34)
Sato, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sato@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="ciad15006"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/notes="Vector: pBluescript SK"
BASE COUNT 12 a 5 c 8 g 9 t
ORIGIN

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Db 11 TGAAGGCGG 20
Search completed: June 23, 2003, 10:10:24
Job time : 1548.89 secs

Query Match 33.3%; Score 10; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAAT 10
Db 16 GCTCTAGAAAT 7

RESULT 15
T74961
LOCUS
DEFINITION
Yc85b03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone
IMAGE:22801 5' similar to SP:A27671 A27671 SPECTRIN ALPHA CHAIN,
NONERYTHROID - RAT ;, mRNA sequence.
T74961
ACCESSION
VERSION
KEYWORDS
SOURCE
T74961.1 GI:691636
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1872

High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, L1N1 This clone is available royalty-free
through L1N1; contact the IMAGE Consortium (info@image.l1n1.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1872 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
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1..34
/organism="Homo sapiens"
/db_xref="GDB:395148"
/db_xref="taxon:9606"
/clone="IMAGE:22801"
/clone_lib="Soares infant brain 1N1B"
/sex="Female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5];
AACTGGAGAAATTCGGCCGCGGAGGAAATTTTTTTTTTTT 3';
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 7 a 6 c 13 g 8 t
ORIGIN

Query Match 33.3%; Score 10; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAAGGCGG 26
|||||||

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 45.5378 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-8
Perfect score: 30
Sequence: 1 GCTCTAGTAATGAACGGTGGAGCGGCGAGG 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A-COMB.seq.*
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4: /cgn2_6/prodata/2/ina/6B-COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUS-COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	US-08-770-565-8
2	29	96.7	30	2	US-08-833-377-6
3	23	76.7	27	2	US-08-770-565-26
4	22	73.3	26	1	US-08-330-123A-23
5	22	73.3	26	1	US-08-482-115B-23
6	22	73.3	26	2	US-08-660-678A-23
7	22	73.3	26	2	US-08-710-249-26
8	22	73.3	26	2	US-08-485-778-19
9	22	73.3	26	2	US-08-472-802C-24
10	22	73.3	26	3	US-08-520-550A-19
11	22	73.3	26	3	US-08-998-443-23
12	22	73.3	26	4	US-08-974-549A-598
13	22	73.3	26	4	US-09-060-523-23
14	22	73.3	26	4	US-09-220-157A-26
15	22	73.3	26	4	US-09-286-959B-4
16	22	73.3	26	4	US-09-580-517-23
17	19	63.3	19	2	US-08-770-565-9
18	16.8	56.0	27	3	US-08-630-172-24
19	16.8	56.0	27	4	US-09-375-419-24
20	16.4	54.7	18	4	US-08-974-549A-543
21	15.8	52.7	30	4	US-08-846-247-13
22	15.6	52.0	50	2	US-08-448-418-31
23	15.4	51.3	31	4	US-09-513-838-3
24	15.4	51.3	42	1	US-08-439-813-2
25	15.4	51.3	42	5	PCR-US96-05291A-2
26	15	50.0	15	2	US-08-770-565-10
27	15	50.0	25	1	US-08-629-939-8

28	15	50.0	25	1	US-08-759-873-8	Sequence 8, Appli
29	14.6	48.7	40	1	US-08-411-795B-255	Sequence 255, App
30	14.6	48.7	40	1	US-08-469-319A-255	Sequence 255, App
31	14.6	48.7	40	4	US-08-764-114-255	Sequence 255, App
32	14.6	48.7	40	4	US-08-469-419-255	Sequence 255, App
33	14.6	48.7	41	1	US-08-411-795B-234	Sequence 234, App
34	14.6	48.7	41	1	US-08-469-319A-234	Sequence 234, App
35	14.6	48.7	41	4	US-08-764-114-234	Sequence 234, App
36	14.6	48.7	41	4	US-08-469-419-234	Sequence 234, App
37	14.6	48.7	45	1	US-08-411-795B-409	Sequence 409, App
38	14.6	48.7	45	1	US-08-469-319A-409	Sequence 409, App
39	14.6	48.7	45	4	US-08-764-114-409	Sequence 409, App
40	14.6	48.7	45	4	US-08-469-419-409	Sequence 409, App
41	14.4	48.0	37	1	US-08-591-492-17	Sequence 17, Appli
42	14.2	47.3	48	2	US-08-729-955A-9	Sequence 9, Appli
43	14.2	47.3	49	4	US-09-538-709-931	Sequence 931, App
44	14	46.7	28	4	US-09-033-333-18	Sequence 18, Appl
45	14	46.7	28	4	US-09-033-428-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-8
; Sequence 8, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00230005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-8

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred.No. 4.3e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGTAATGAACGGTGGAGCGGCGAGG 30

Db 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

US-08-833-377-6

Sequence 6, Application US/08833377

Patent No. 5968506

GENERAL INFORMATION:

APPLICANT: Weinrich, Scott L.

APPLICANT: Atkinson III, Edward M.

APPLICANT: Lichtsteiner, Serge P.

APPLICANT: Vasserot, Alain P.

APPLICANT: Pruzan, Ronald A.

APPLICANT: Kealey, James T.

TITLE OF INVENTION: Purified Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,377

FILING DATE: 04-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/510,736

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-001110US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: modified_base

LOCATION: 1

OTHER INFORMATION: /mod base= OTHER

OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"

FEATURE:

NAME/KEY: -

LOCATION: 1..30

OTHER INFORMATION: /note= "Oligo 14"

US-08-833-377-6

Query Match 96.7%; Score 29; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTAGATGAACGGTGGAGCGGCAGG 30

Db 2 CTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 3

US-08-770-565-26

Sequence 26, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-26

Query Match 76.7%; Score 23; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.065;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGAGG 23

Db 5 GCTCTAGATGAACGGTGGAGG 27

RESULT 4

US-08-330-123A-23

Sequence 23, Application US/08330123A

Patent No. 5583016

GENERAL INFORMATION:

APPLICANT: VILLEPONTEAU, Bryant

APPLICANT: FENG, Junli

APPLICANT: FUNK, Walter

APPLICANT: ANDREWS, William H.

TITLE OF INVENTION: HUMAN TELOMERASE

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACGGTGAAG 22
|||||
DB 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 5
US-08-482-115B-23
Sequence 23, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Vilpenteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACGGTGAAG 22
|||||
DB 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 6
US-08-660-678A-23
Sequence 23, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Vilpenteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACGGTGAAG 22

```

db      5 GCTCTAGATGAACGGTGAAG 26
|||||
RESULT 7
US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; Tissue Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred.No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0

QY      1 GCTCTAGATGAACGGTGAAG 22
|||||
DB      5 GCTCTAGATGAACGGTGAAG 26
|||||

RESULT 8
US-08-485-778-19
; Sequence 19, Application US/08485778
; Patent No. 5878979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Grainger, Carol

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGAAG 22
|||||
Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 10
US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-19

Query Match 73.3%; Score 22; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGAAG 22
|||||
Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 11
US-08-998-443-23
Sequence 23, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 73.3%; Score 22; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGAG 22
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 12
US-08-974-549A-598
Sequence 598, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGAG 22
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 13
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Strella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 14

US-09-220-157A-26
; Sequence 26, Application US/09220157A
; Patent No. 6300110

; GENERAL INFORMATION:

; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/220.157A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/710.249

; FILING DATE: 13-SEP-1996

; APPLICATION NUMBER: US 08/583.808

; FILING DATE: 05-JAN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/003.492

; FILING DATE: 08-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 015389-001220US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-09-220-157A-26

Query Match

73.3%; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

RESULT 15

US-09-286-959B-4

; Sequence 4, Application US/09286959B

; Patent No. 6300131

; GENERAL INFORMATION:

; APPLICANT: Johns Hopkins University

; APPLICANT: Greider, Carol W.

; APPLICANT: Le, Siyuan

; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS

; FILE REFERENCE: 07265/157001

; CURRENT APPLICATION NUMBER: US/09/286.959B

; CURRENT FILING DATE: 1999-04-06

; PRIOR APPLICATION NUMBER: 60/080.783

; PRIOR FILING DATE: 1998-04-06

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-09-286-959B-4

Query Match

73.3%; Score 22; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGAAG 22
Db 5 GCTCTAGAAATGAACGGTGAAG 26

Search completed: June 25, 2003, 00:24:39

Job time : 46.5378 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 91.1952 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30

Sequence: 1 GCTTAGAATGACGGTGAAGCGGCAGG 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	73.3	26	9	US-10-044-692-312 Sequence 312, App
2	22	73.3	26	9	US-10-044-539-312 Sequence 312, App
3	22	73.3	26	10	US-09-057-351-23 Sequence 23, Appl
4	15.8	52.7	30	9	US-09-852-416-31 Sequence 31, Appl
5	15.8	52.7	30	9	US-10-096-789-13 Sequence 13, Appl
6	15.8	52.7	30	9	US-10-096-790-10 Sequence 10, Appl
7	15.8	52.7	30	10	US-09-859-854-31 Sequence 31, Appl
8	15.4	51.3	31	9	US-10-139-483-3 Sequence 3, Appl
9	14.6	48.7	40	9	US-10-090-182A-255 Sequence 255, App
10	14.6	48.7	41	9	US-10-090-182A-234 Sequence 234, App
11	14.6	48.7	45	9	US-10-090-182A-409 Sequence 409, App
12	14.2	47.3	25	9	US-10-098-263B-51583 Sequence 51583, A
13	14	46.7	25	9	US-10-098-263B-81514 Sequence 81514, A
14	14	46.7	25	9	US-10-098-263B-105334 Sequence 105334, A
15	14	46.7	28	9	US-09-898-883-19 Sequence 19, Appl
16	14	46.7	28	9	US-10-045-116-15 Sequence 16, Appl
17	14	46.7	28	9	US-10-222-478-18 Sequence 18, Appl
18	14	46.7	28	10	US-09-814-292-39 Sequence 39, Appl
19	14	46.7	28	10	US-09-875-228-25 Sequence 25, Appl

Sequence 21, Appl
Sequence 64498, A
Sequence 56, Appl
Sequence 67, Appl
Sequence 56, Appl
Sequence 67, Appl
Sequence 7103, Appl
Sequence 11, Appl
Sequence 4633, Appl
Sequence 4634, Appl
Sequence 31404, A
Sequence 72147, A
Sequence 25, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 235, Appl
Sequence 50, Appl
Sequence 8975, Appl
Sequence 13825, A
Sequence 27359, A
Sequence 27360, A
Sequence 93148, A
Sequence 6, Appl
Sequence 17930, A
Sequence 19, Appl
Sequence 77, Appl

US-10-062-809-21
US-10-098-263B-64498
US-10-033-297-56
US-10-081-806-67
US-09-940-244-56
US-09-982-667-67
US-09-848-754A-7103
US-09-780-566-11
US-10-215-112-4633
US-10-215-112-4634
US-10-098-263B-31404
US-10-098-263B-72147
US-10-012-013-25
US-09-819-097-5
US-09-748-451-13
US-10-090-182A-235
US-10-086-156-50
US-10-215-112-8975
US-10-215-112-13825
US-10-098-263B-27359
US-10-098-263B-27360
US-10-098-263B-93148
US-09-850-964-6
US-10-098-263B-17930
US-09-952-522B-19
US-10-273-541-77

ALIGNMENTS

RESULT 1

US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

us-08-770-564a-8.rnpb

Fri Jun 27 07:43:12 2003

```

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAG 22
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeganteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAG 22
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 2
US-10-044-539-312
; Sequence 312, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match      73.3%; Score 22; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGAAG 22
    |||||
Db 5 GCTCTAGAATGAACGGTGAAG 26

RESULT 4
US-09-852-416-31
; Sequence 31,, Application US/09852416
; Publication No. US20030040084A1
; GENERAL INFORMATION:
; APPLICANT: Khosla, Chaitan
; APPLICANT: Ashley, Gary
; APPLICANT: Fu, Hong
; APPLICANT: Kao, Camilla M.
; APPLICANT: McDaniel, Robert
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; TITLE OF INVENTION: PRODUCED USING A MODULAR PKS GENE CLUSTER AS SCAFFOLD
; FILE REFERENCE: 30062-20005.02
; CURRENT APPLICATION NUMBER: US/09/852,416
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/859,854
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/US98/08792
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/076,919
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/846,247
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: 08/486,645
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/238,811
; PRIOR FILING DATE: 1994-05-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Module rapDH/ER/KR1 (reverse) Primer pairs used
; OTHER INFORMATION: for PCR amplification of rapamycin PKS cassettes.
US-09-852-416-31

Query Match      52.7%; Score 15.8; DB 9; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTAGAATGAACGGTGAAGCGGCAG 29
    |||||
Db 4 TCTAGAATCAACGGTGAAGCAGCCG 30

RESULT 5
US-10-096-789-13
; Sequence 13, Application US/10096789
; Publication No. US2003007760A1
; GENERAL INFORMATION:
; APPLICANT: Khosla, Chaitan
; APPLICANT: Ashley, Gary
; APPLICANT: Fu, Hong
; APPLICANT: McDaniel, Robert
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; TITLE OF INVENTION: PRODUCED USING A MODULAR PKS GENE CLUSTER
; AS SCAFFOLD
US-10-096-789-13

Query Match      52.7%; Score 15.8; DB 9; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTAGAATGAACGGTGAAGCGGCAG 29
    |||||
Db 4 TCTAGAATCAACGGTGAAGCAGCCG 30

RESULT 6
US-10-096-790-10
; Sequence 10, Application US/10096790
; Publication No. US20030077707A1
; GENERAL INFORMATION:
; APPLICANT: Kusan Biosciences, Inc.
; APPLICANT: Khosla, Chaitan
; APPLICANT: Kao, Camilla
; TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES
; TITLE OF INVENTION: PRODUCED USING A MODULAR PKS GENE CLUSTER AS SCAFFOLD
; FILE REFERENCE: 30062-20005.03
; CURRENT APPLICATION NUMBER: US/10/096,790
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/076,919
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/003,338
; PRIOR FILING DATE: 1995-07-06
; PRIOR APPLICATION NUMBER: US 08/846,247
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: US 08/486,645
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/238,811
; PRIOR FILING DATE: 1994-05-06
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/ PRIOR APPLICATION NUMBER: US/08/164,301
/ PRIOR FILING DATE: 1993-12-08
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer rapDH/ER/KR1 (right half) (reverse)
US-10-096-790-10

Query Match      52.7%; Score 15.8; DB 9; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTAGAAATGACCGGTGGAAGCGGCAG 29
    |||||
Db 4 TCTAGAAATCACCGGTAGAGACGCCCG 30

RESULT 7
US-08-859-854-31
/ Sequence 31, Application US/09859854
/ Patent No. US20020068332A1
/ GENERAL INFORMATION:
/ APPLICANT: PKhosla, Chaitan
/ APPLICANT: Ashley, Gary
/ APPLICANT: Fu, Hong
/ APPLICANT: Kao, Camilla M.
/ APPLICANT: McDaniel, Robert
/ TITLE OF INVENTION: COMBINATORIAL POLYPEPTIDE LIBRARIES
/ FILE REFERENCE: 30062-20005.02
/ CURRENT APPLICATION NUMBER: US/09/859,854
/ CURRENT FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: PCT/US98/08792
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/076,919
/ PRIOR FILING DATE: 1998-03-05
/ PRIOR APPLICATION NUMBER: 08/846,247
/ PRIOR FILING DATE: 1997-04-30
/ PRIOR APPLICATION NUMBER: 08/486,645
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/238,811
/ PRIOR FILING DATE: 1994-05-06
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 31
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Module rapDH/ER/KR1 (reverse) Primer pairs used
/ OTHER INFORMATION: for PCR amplification of rapamycin PKS cassettes.
US-09-859-854-31

Query Match      52.7%; Score 15.8; DB 10; Length 30;
Best Local Similarity 74.1%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTAGAAATGACCGGTGGAAGCGGCAG 29
    |||||
Db 4 TCTAGAAATCACCGGTAGAGACGCCCG 30

RESULT 8
US-10-139-483-3
/ Sequence 3, Application US/10139483
/ Publication No. US20030055266A1
/ GENERAL INFORMATION:
/ APPLICANT: Beeley, Nigel R
/ APPLICANT: Behan, Dominic P

/ APPLICANT: Chalmers, Derek T
/ APPLICANT: Menzaghi, Frederique
/ APPLICANT: Strah-Pleyret, Sonja
/ TITLE OF INVENTION: Small Molecule Modulators Of G Protein-Coupled Receptor
/ TITLE OF INVENTION: Six
/ FILE REFERENCE: AREN0058
/ CURRENT APPLICATION NUMBER: US/10/139,483
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US/09/513,838
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/364,425
/ PRIOR FILING DATE: 1999-07-30
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 31
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-139-483-3

Query Match      51.3%; Score 15.4; DB 9; Length 31;
Best Local Similarity 76.0%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CTCTAGAAATGACCGGTGGAAGCGCG 26
    |||||
Db 4 CTCTAGAAATGACCGGTGCAAAATCCG 28

RESULT 9
US-10-090-182A-255
/ Sequence 255, Application US/10090182A
/ Publication No. US20030103936A1
/ GENERAL INFORMATION:
/ APPLICANT: Abrams, Mark A.
/ APPLICANT: Bauer, S. C.
/ APPLICANT: Braford-Goldberg, Sarah R.
/ APPLICANT: Caparon, Mairé H.
/ APPLICANT: Easton, Alan M.
/ APPLICANT: Klein, Barbara K.
/ APPLICANT: McKearn, John P.
/ APPLICANT: Olin, Peter O.
/ APPLICANT: Paik, Kuman
/ APPLICANT: Thomas, John W.
/ TITLE OF INVENTION: Methods of Ex-vivo Expansion of
/ Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
/ Mutation Polypeptides
/ NUMBER OF SEQUENCES: 415
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
/ STREET: 800 N. Lindbergh Blvd.
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63167
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/090,182A
/ FILING DATE: 03-Apr-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/764,114
/ FILING DATE: 09-DEC-1996
/ APPLICATION NUMBER: US 07/981,044
/ FILING DATE: 24-NOV-1992
/ APPLICATION NUMBER: PCT/US93/11197
/ FILING DATE: 22-NOV-1993
/ APPLICATION NUMBER: 08/411,795
```

;; FILING DATE: 04-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: S. Christopher Bauer
;; REGISTRATION NUMBER: 42,305
;; REFERENCE/DOCKET NUMBER: C2713/12
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (636)737-6257
;; TELEFAX: (736)737-6257
;; INFORMATION FOR SEQ ID NO: 255:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (synthetic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 255:
US-10-090-182A-255

Query Match 48.7%; Score 14.6; DB 9; Length 40;
Best Local Similarity 81.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGAA 21
||||| ||||| ||||| ||||| |||||
Db 12 GCTCTATATGATCGATGAAA 32
||||| ||||| ||||| ||||| |||||

RESULT 10
US-10-090-182A-234
; Sequence 234, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olines, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides
; NUMBER OF SEQUENCES: 415
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
; Corporate Patent Dept. Mail Zone 04E
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/090,182A
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/764,114
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; APPLICATION NUMBER: PCT/US93/11197
; FILING DATE: 22-NOV-1993
; APPLICATION NUMBER: 08/411,795
; FILING DATE: 04-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305

;; NAME: S. Christopher Bauer
;; REGISTRATION NUMBER: 42,305
;; REFERENCE/DOCKET NUMBER: C2713/12
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (636)737-6257
;; TELEFAX: (736)737-6257
;; INFORMATION FOR SEQ ID NO: 234:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 41 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (synthetic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 234:
US-10-090-182A-234

Query Match 48.7%; Score 14.6; DB 9; Length 41;
Best Local Similarity 81.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGAA 21
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Db 12 GCTCTATATGATCGATGAAA 32
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RESULT 11
US-10-090-182A-409/c
; Sequence 409, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olines, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides
; NUMBER OF SEQUENCES: 415
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
; Corporate Patent Dept. Mail Zone 04E
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/090,182A
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/764,114
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; APPLICATION NUMBER: PCT/US93/11197
; FILING DATE: 22-NOV-1993
; APPLICATION NUMBER: 08/411,795
; FILING DATE: 04-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305

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; REFERENCE/DOCKET NUMBER: C2713/12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (636)737-6257
; TELEFAX: (736)737-6257
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: DNA (synthetic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 409:
US-10-090-182A-409

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Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAA 21
Db 38 GCTCTATAATGATCGATGAA 18

RESULT 12
US-10-098-263B-51583
; Sequence 51583, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-51583

Query Match 47.3%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTCTAGATGAACGGTGGGA 20
Db 7 CTCTAGAGTCAACGCTGGA 25

RESULT 13
US-10-098-263B-81514/c
; Sequence 81514, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81514
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-81514

Query Match 46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 24 CTCTAGAAGGTACGGGTAGG 3

RESULT 14
US-10-098-263B-105334/c
; Sequence 105334, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105334

Query Match 46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTAGAATGAACGGTGAAGCG 25
Db 23 CTAGACTGGACTGGGTAGTCG 2

RESULT 15
US-09-898-883-19
; Sequence 19, Application US/09898883
; Patent No. US20020164799A1
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,883
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIEZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
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;
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-898-883-19

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Query Match      46.7%; Score 14; DB 9; Length 28;
Best Local Similarity 77.3%; Pred. NO. 4.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db      6 AATTAACGTGTGAAGGTGGGAG 27

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 2545.58 Seconds
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296.308 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30
Sequence: 1 GCTCTAGATGAACGGTGAAGCGGCAGG 30

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	30	100.0	30	11	US-08-770-564A-8
4	30	100.0	30	21	US-09-540-119B-10
5	30	100.0	30	28	US-09-717-828A-5
6	30	100.0	30	28	US-09-717-828B-5
7	30	100.0	30	28	US-09-717-829A-5
8	30	100.0	30	34	US-09-903-461-2
9	23	76.7	27	1	PCT-US97-23619-26
10	22	73.3	25	16	US-09-250-336A-4
11	22	73.3	25	25	US-09-642-177-4
12	22	73.3	26	1	PCT-US96-14679-27
13	22	73.3	26	1	PCT-US96-14679A-27
14	22	73.3	26	1	PCT-US99-03302-4
15	22	73.3	26	1	PCT-US99-07533-4
16	22	73.3	26	1	PCT-US99-07533-4
17	22	73.3	26	6	US-08-272-102-23
18	22	73.3	26	7	US-08-381-524-19
19	22	73.3	26	8	US-08-472-802A-24
20	22	73.3	26	8	US-08-472-802B-24
21	22	73.3	26	8	US-08-482-115A-23

US-08-770-564A-8
; Sequence 8, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: S14
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-8

Query Match 100.0%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 4
US-09-540-119B-10
; Sequence 10, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-10

Query Match 100.0%; Score 30; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 5
US-09-717-828A-5
; Sequence 5, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Alain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-5

Query Match 100.0%; Score 30; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30
DB 1 GCTCTAGATGAACGGTGGAGCGGCAGG 30

RESULT 6
US-09-717-828B-5
; Sequence 5, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Alain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
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; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature

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; TYPE: DNA
; ORGANISM: Artificial Sequence

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Db 5 GCTCTAGATGAACGGTGAAG 27
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RESULT 10
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; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 73.3%; Score 22; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
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Db 4 GCTCTAGATGAACGGTGAAG 25
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RESULT 11
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 73.3%; Score 22; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22

Db 4 GCTCTAGATGAACGGTGAAG 25
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RESULT 12
PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
|||||

Db 5 GCTCTAGATGAACGGTGAAG 26
|||||

RESULT 13
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.

Fri Jun 27 07:43:13 2003

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; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US96-14679A-27

; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; PCT-US99-07533-4

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
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DB 5 GCTCTAGATGAACGGTGAAG 26
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Job time : 2547.19 secs

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RESULT 14
PCT-US99-03302-4
; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamberg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; TITLE OF INVENTION: and Assessment of Disease Stage and Prognosis
; FILE REFERENCE: 1489US 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3c,
; OTHER INFORMATION: synthesized, Gibco-BRL
; PCT-US99-03302-4

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
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DB 5 GCTCTAGATGAACGGTGAAG 26
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RESULT 15
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; Sequence 4, Application PC/TUS9907533
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 716.653 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-8
Perfect score: 30
Sequence: 1 GCTCTAGATGAACCGTGAAGCGCGCAGG 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New.*

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13: /cgn2_6/ptodata/1/pna/US18_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	30	10	US-10-330-872-5
2	30	100.0	30	10	US-10-330-872A-5
3	23	76.7	23	1	PCT-US03-04088-520
4	22	73.3	23	1	PCT-US03-04088-529
5	22	73.3	26	6	US-09-721-456-598
6	22	73.3	26	9	US-10-325-810-598
7	22	73.3	26	9	US-10-359-935-23
8	21	70.0	21	1	PCT-US03-04088-587
9	21	70.0	21	1	PCT-US03-04088-521
10	20	66.7	21	1	PCT-US03-04088-592
11	19	63.3	19	1	PCT-US03-04088-14
12	19	63.3	19	1	PCT-US03-04088-257
13	19	63.3	19	1	PCT-US03-04088-278
14	19	63.3	21	1	PCT-US03-04088-538
15	19	63.3	21	1	PCT-US03-04088-539
16	19	63.3	21	1	PCT-US03-04088-542
17	19	63.3	21	1	PCT-US03-04088-543
18	19	63.3	21	1	PCT-US03-04088-546
19	19	63.3	21	1	PCT-US03-04088-547
20	19	63.3	21	1	PCT-US03-04088-550

21 19 63.3 21 1 PCT-US03-04088-551 Sequence 551, App
c 22 19 63.3 21 1 PCT-US03-04088-554 Sequence 554, App
c 23 19 63.3 21 1 PCT-US03-04088-555 Sequence 555, App
24 19 63.3 21 1 PCT-US03-04088-558 Sequence 558, App
25 19 63.3 21 1 PCT-US03-04088-559 Sequence 559, App
26 16.8 56.0 38 12 US-60-432-699-268 Sequence 268, App
27 16.4 54.7 18 6 US-09-721-456-543 Sequence 543, App
28 16.4 54.7 18 9 US-10-325-810-543 Sequence 543, App
29 16.2 54.0 25 9 US-10-355-577-381773 Sequence 381773,
30 16.2 54.0 25 12 US-60-427-836-119888 Sequence 119888,
c 31 16 53.3 25 12 US-60-417-190-121065 Sequence 121065,
c 32 16 53.3 25 12 US-60-417-190-121066 Sequence 121066,
c 33 16 53.3 25 13 US-60-470-475-106304 Sequence 106304,
34 15.8 52.7 30 9 US-10-355-577-751232 Sequence 751232,
35 15.8 52.7 30 10 US-10-213-926-31 Sequence 31, Appl
36 15.6 52.0 25 7 US-09-954-445A-52770 Sequence 52770, A
c 37 15.6 52.0 25 12 US-60-427-808-483204 Sequence 483204,
38 15.4 51.3 25 9 US-10-355-577-775297 Sequence 775297,
c 39 15.4 51.3 25 9 US-10-355-577-775298 Sequence 775298,
c 40 15.2 50.7 25 12 US-60-427-808-738286 Sequence 738286,
c 41 15.2 50.7 50 1 PCT-US03-13015-881 Sequence 881, App
c 42 15.2 50.7 50 9 US-10-325-899-5782 Sequence 5782, App
c 43 15.2 50.7 25 9 US-10-355-577-906233 Sequence 906233,
c 44 15 50.0 25 9 US-10-355-577-906236 Sequence 906236,
c 45 15 50.0 25 9 US-10-355-577-906236 Sequence 906236,

ALIGNMENTS

RESULT 1
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACCGTGAAGCGCGCAGG 30
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Db 1 GCTCTAGATGAACCGTGAAGCGCGCAGG 30
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RESULT 2
US-10-330-872A-5
; Sequence 5, Application US/10330872A

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; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-330-872A-5

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGGAGGCGGAGG 30
Db 1 GCTCTAGATGAACGGTGGGAGGCGGAGG 30

RESULT 3
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-529

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGGGAGGCGGAGG 30
Db 23 ATGAACGGTGGGAGGCGGAGG 2

RESULT 5
PCT-US03-04088-529
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727

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; OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 76.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGGAGG 23
Db 23 GCTCTAGATGAACGGTGGGAGG 1

RESULT 4
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; Sequence 529, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 529
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-529

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGGGAGGCGGAGG 30
Db 23 ATGAACGGTGGGAGGCGGAGG 2

RESULT 5
PCT-US03-04088-529
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727

```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-Nov-1997
 APPLICATION NUMBER: US/08/724,643
 FILING DATE: 01-Oct-1996
 APPLICATION NUMBER: US/08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US/08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US/08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US/08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US/08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US/08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 598:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..26
 OTHER INFORMATION: /note= "R3c primer"
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 US-09-721-456-598
 Query Match 73.3%; Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGAAG 22
 DB 5 GCTCTAGATGAACGGTGAAG 26
 RESULT 6
 US-10-325-810-598
 ; Sequence 598, Application US/10325810
 ; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,810
 FILING DATE: 20-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181
 FILING DATE: 29-Sep-1997
 APPLICATION NUMBER: US/08/724,643
 FILING DATE: 01-Oct-1996
 APPLICATION NUMBER: US/08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US/08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US/08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US/08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US/08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US/08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenius, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 598:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..26
 OTHER INFORMATION: /note= "R3c primer"
 SEQUENCE DESCRIPTION: SEQ ID NO: 598:
 US-10-325-810-598
 Query Match 73.3%; Score 22; DB 9; Length 26;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGAAG 22
 DB 5 GCTCTAGATGAACGGTGAAG 26

Db 5 GCTCTAGATGAACGGTGAAG 26

RESULT 7

US-10-359-935-23
; Sequence 23, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; Feng, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 73.3%; Score 22; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACGGTGAAG 22
|||||
Db 5 GCTCTAGATGAACGGTGAAG 26
RESULT 8
PCT-US03-04088-587/c
; Sequence 587, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)

; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 587
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-587

Query Match 70.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 ATGAACGGTGAACGGCGCAG 29
|||||
Db 21 ATGAACGGTGAACGGCGCAG 1

RESULT 9

PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial

;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
;; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 70.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGGAA 21
|||||:|||||:|||||:|||||
Db 21 GCTCTAGAAATGAACGGTGGAA 1

RESULT 10
PCT-US03-04088-592
; Sequence 592, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
PCT-US03-04088-592

Query Match 66.7%; Score 20; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 52;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGGTGGAGCGGCAGG 30
|||||:|||||:|||||:|||||
Db 1 GAACGGUGGAGCGGCAGG 20

RESULT 11
PCT-US03-04088-14/c
; Sequence 14, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088

;; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-14

Query Match 63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGGAGCGGC 27
|||||:|||||:|||||:|||||
Db 19 ATGAACGGTGGAGCGGC 1

RESULT 12
PCT-US03-04088-257/c
; Sequence 257, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 257
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

```

; OTHER INFORMATION: region
PCT-US03-04088-257

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAACGCTGAAGCGGCAG 29
Db 19 GAACGCTGAAGCGGCAG 1

RESULT 13
PCT-US03-04088-278
; Sequence 278, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGCTGAAGCGGC 27
Db 1 AUGAACGUGGAGCGGC 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
PCT-US03-04088-278

Query Match      63.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAACGGTGGA 21
Db 19 TCTAGATGAACGGTGGA 1

RESULT 15
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
PCT-US03-04088-278

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; OTHER INFORMATION: Description of Artificial Sequence:  sRNA sense region
; FEATURE:
; NAME/KEY:  misc.feature
; LOCATION: (20)..(21)
; OTHER INFORMATION:  n stands for thymidine
PCT-US03-04088-539
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Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCTAGATGAACGGTGG 19
      |||||||
Db      19  GCTCTAGATGAACGGTGG 1
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-7
Perfect score: 20
Sequence: 1 CCAACTCTTCGGGTGGCAG 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
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- 14: gb_vi.*
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- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sv.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AR063831	AR063831 Sequence
2	20	100.0	30	6	AR063829	AR063829 Sequence
3	13	65.0	46	6	I28704	I28704 Sequence 7
4	12	60.0	26	6	AX109246	AX109246 Sequence
5	11	55.0	20	6	A30766	A30766 Artificial
6	11	55.0	20	12	AB069392	AB069392 Synthetic
7	11	55.0	21	6	A37934	A37934 Sequence 12
8	11	55.0	24	6	AX445639	AX445639 Sequence
9	11	55.0	25	6	AX115384	AX115384 Sequence
10	11	55.0	30	6	AR142066	AR142066 Sequence
11	11	55.0	30	6	I59933	I59933 Sequence 60
12	11	55.0	30	6	I86791	I86791 Sequence 60
13	11	55.0	30	6	I95816	I95816 Sequence 60
14	11	55.0	36	6	AX060321	AX060321 Sequence
15	11	55.0	43	6	AX484473	AX484473 Sequence
16	11	55.0	48	6	AX068199	AX068199 Sequence
17	11	55.0	48	6	AX068203	AX068203 Sequence
18	10	50.0	11	6	I18772	I18772 Sequence 3
19	10	50.0	11	6	I95608	I95608 Sequence 3
20	10	50.0	15	6	AR056247	AR056247 Sequence
21	10	50.0	15	6	AR114005	AR114005 Sequence
22	10	50.0	18	6	AR008099	AR008099 Sequence
23	10	50.0	18	6	AX378621	AX378621 Sequence
24	10	50.0	20	4	BOVINE20	D83300 Bovine DNA
25	10	50.0	20	6	A30767	A30767 Artificial
26	10	50.0	20	6	AR063830	AR063830 Sequence
27	10	50.0	20	6	AR068779	AR068779 Sequence
28	10	50.0	20	6	AR092381	AR092381 Sequence
29	10	50.0	20	6	AR092653	AR092653 Sequence
30	10	50.0	20	6	AR130983	AR130983 Sequence
31	10	50.0	20	6	AR139457	AR139457 Sequence
32	10	50.0	20	6	AX293905	AX293905 Sequence
33	10	50.0	20	6	AX294358	AX294358 Sequence
34	10	50.0	20	6	AX294843	AX294843 Sequence
35	10	50.0	20	6	AX363221	AX363221 Sequence
36	10	50.0	20	6	E22563	E22563 Process for
37	10	50.0	20	6	E25721	E25721 Method for
38	10	50.0	20	12	AB069038	AB069038 Synthetic
39	10	50.0	21	6	AX033200	AX033200 Sequence
40	10	50.0	21	6	AX350215	AX350215 Sequence
41	10	50.0	22	4	DOG34801	L24234 Dog (Clone)
42	10	50.0	22	6	AX399648	AX399648 Sequence
43	10	50.0	22	6	AX399649	AX399649 Sequence
44	10	50.0	22	6	AX399650	AX399650 Sequence
45	10	50.0	23	6	AX253560	AX253560 Sequence

ALIGNMENTS

Result 1	Score	Query Match	Length	DB	ID	Description
AR063831	AR063831	Sequence 7	from patent US 5846723.	20 bp	DNA	linear PAT 29-SBP-1999
LOCUS	AR063831	Sequence 7	from patent US 5846723.	20 bp	DNA	linear PAT 29-SBP-1999
DEFINITION	AR063831	Sequence 7	from patent US 5846723.	20 bp	DNA	linear PAT 29-SBP-1999
ACCESSION	AR063831	Sequence 7	from patent US 5846723.	20 bp	DNA	linear PAT 29-SBP-1999
VERSION	AR063831.1	GI:5993139				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.					
TITLE	Methods for detecting the RNA component of telomerase					
JOURNAL	Patent: US 5846723-A 7 08-DEC-1998;					
FEATURES	Location/Qualifiers					

AUTHORS Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36.
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
REFERENCE 2 (bases 1 to 20)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES Location/Qualifiers
 source
 1..20
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 misc_feature
 1..20
 /note="forward primer for human STS sts-stSG28879 at 1p36 sts-stSG28879 obtained from clones B52P16, B32C18, B36214, Human BAC library RPCI-11"
BASE COUNT 4 a 4 c 5 g 7 t
ORIGIN
 Query Match 55.0%; Score 11; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CTCCTCGCGGT 15
Db 15 CTCCTCGCGGT 5
RESULT 7
LOCUS A37934 21 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9408018.
ACCESSION A37934
VERSION A37934.1 GI:2294591
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Varvill, K., Pickersgill, R.W., Gould, G.W., Goodenough, P.W. and Mosely, B.E.
TITLE ALTERATION OF POLYPEPTIDES
JOURNAL Patent: WO 9408018-A 12 14-APR-1994;
 UNILEVER PLC (GB)
COMMENT Other publication GB 2273931 940706
 Other publication JP 8501939T 960305.
FEATURES Location/Qualifiers
 source
 1..21
 /organism="unidentified"
 /db_xref="taxon:32644"
BASE COUNT 8 a 5 c 7 g 1 t
ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TCTTCGCGGTG 16
Db 19 TCTTCGCGGTG 9
RESULT 8
LOCUS AX445639/c 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 2094 from Patent WO0216649.

ACCESSION AX445639
VERSION AX445639.1 GI:21692920
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Gunderson, K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 2094 28-FEB-2002;
 Illumina, Inc. (US)
FEATURES Location/Qualifiers
 source
 1..24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Computer Generated Probe Sequence."
BASE COUNT 4 a 8 c 6 g 6 t
ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CAACTCTTCGC 12
Db 11 CAACTCTTCGC 1
RESULT 9
LOCUS AX115384 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 507 from Patent WO0129262.
ACCESSION AX115384
VERSION AX115384.1 GI:14032326
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 507 28-APR-2001;
 Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
 source
 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"
BASE COUNT 5 a 10 c 2 g 8 t
ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACTCTTCG 11
Db 12 CCAACTCTTCG 22
RESULT 10
LOCUS AR142066/c 30 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6174668.
ACCESSION AR142066
VERSION AR142066.1 GI:15102366
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Cummins, T.J., Atwood, S. Melissa., Bergmeyer, L., Findlay, J. Bruce., Sutherland, J.W.H. and Kerschner, J.H.

TITLE Diagnostic compositions, elements, methods and test kits for amplification and detection of two or more target DNA's using primers having matched melting temperatures
 JOURNAL Patent: US 6174668-A 60 16-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..30
 BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

Query Match 55.0%; Score 11; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 11

LOCUS 159933/c 30 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 60 from patent US 5654416.
 ACCESSION 159933
 VERSION 159933.1 GI:2478565
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Cummins,T.J., Atwood,S.Melissa., Bergmeyer,L., Findlay,J.Bruce., Sutherland,J.W.H. and Kerschner,J.H.
 TITLE Diagnostic primers and probes
 JOURNAL Patent: US 5654416-A 60 05-AUG-1997;
 FEATURES Location/Qualifiers
 source 1..30
 BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

Query Match 55.0%; Score 11; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 12

LOCUS 186791/c 30 bp DNA linear PAT 10-JUN-1998
 DEFINITION Sequence 60 from patent US 5702901.
 ACCESSION 186791
 VERSION 186791.1 GI:3206509
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Cummins,T.J., Atwood,S.Melissa., Bergmeyer,L., Findlay,J.Bruce., Sutherland,J.W.H. and Kerschner,J.H.
 TITLE Diagnostic compositions, elements, methods and test kits for amplification and detection of two or more DNA's using primers having matched melting temperatures
 JOURNAL Patent: US 5702901-A 60 30-DEC-1997;
 FEATURES Location/Qualifiers
 source 1..30
 BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

Query Match 55.0%; Score 11; DB 6; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 13

LOCUS 195816/c 30 bp DNA linear PAT 01-DEC-1998
 DEFINITION Sequence 60 from patent US 5733751.
 ACCESSION 195816
 VERSION 195816.1 GI:3940286
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Cummins,T.J., Atwood,S.Melissa., Bergmeyer,L., Findlay,J.Bruce., Sutherland,J.W.H. and Kerschner,J.H.
 TITLE Diagnostic compositions, elements, methods and test kits for amplification and detection of two or more DNA's using primers having matched melting temperatures
 JOURNAL Patent: US 5733751-A 60 31-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..30
 BASE COUNT 5 a 14 c 7 g 4 t

ORIGIN /organism="unknown"

Query Match 55.0%; Score 11; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 21 CGCGGTGGCAG 11

RESULT 14

LOCUS AX060321 36 bp DNA linear PAT 22-JAN-2001
 DEFINITION Sequence 29 from Patent WO0078802.
 ACCESSION AX060321
 VERSION AX060321.1 GI:12405810
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Shinkets,R.A., Fernandes,E., Vernet,C., Yang,M., Boldog,F.L. and Hermann,J.L.
 TITLE Secreted polypeptides and corresponding polynucleotides
 JOURNAL Patent: WO 0078802-A 29 28-DEC-2000;
 FEATURES Location/Qualifiers
 source 1..36
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="chemically synthesized"

BASE COUNT 7 a 12 c 12 g 5 t

ORIGIN /note="chemically synthesized"

Query Match 55.0%; Score 11; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20

Db 20 CGCGGTGGCAG 30

```

RESULT 15
AX484473
LOCUS AX484473 43 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1773 from Patent WO02053728.
ACCESSION AX484473
VERSION AX484473.1 GI:22318825
KEYWORDS
SOURCE
ORGANISM
Candida albicans.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
AUTHORS Gene disruption methodologies for drug target discovery
TITLE Patent: WO 02053728-A 1773 11-JUL-2002;
JOURNAL Elitra Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source
1..43
/organism="Candida albicans"
/db_xref="taxon:5476"
BASE COUNT 18 a 8 c 7 g 10 t
ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCG 11
| | | | | | | | | |
Db 28 CCAACTCTTCG 38

```

Search completed: June 23, 2003, 06:34:18
Job time : 235.051 secs

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XX OS Synthetic.
XX DN WO200216649-A2.
XX PD 28-FEB-2002.
XX PF 27-AUG-2001; 2001WO-US26519.
XX PR 25-AUG-2000; 2000US-27948P.
XX PR 23-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PT different specific capture probes -
XX PS Claim 1; Page 189; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,
XX CC which further comprises detecting the presence of the modified target
XX CC nucleic acid.
XX SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 55.0%; Score 11; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAACTCTTCGC 12
Db 14 CAACTCTTCGC 24

Search completed: June 23, 2003, 05:43:37
Job time : 134.216 secs

```

CC employed to screen gene libraries to identify DKG reductases or cross
 CC reactive activities. DKGR nucleic acids may be sequenced and subjected to
 CC site specific mutagenesis to develop modified DKGR with desired
 CC properties that are absent or less pronounced in the wild-type proteins,
 CC such as greater catalytic efficiency, stability to heat, solvent
 CC tolerance, NADH dependent activity and different optimum pH. The sequence
 CC presented is the PCR primer, 2815, used to amplify
 CC 2,5-diketo-D-gluconic acid reductase d (DKGRd) gene (clone pi-28) from
 CC DNA extracted from soil samples.

XX Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 other;

Query Match 55.0%; Score 11; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGT 15

Db 10 CTCTTCGCGGT 20

RESULT 13

ABQ02087/c

ID ABQ02087 standard; DNA; 24 BP.

XX

AC ABQ02087;

XX

DT 11-JUN-2002 (first entry)

XX

DE Oligonucleotide adapter/capture probe 2078.

XX

KW Oligonucleotide array; adapter sequence; probe; ss.

XX

OS Synthetic.

XX

XX WO200216649-A2.

XX

XX 28-FEB-2002.

XX

XX 27-AUG-2001; 2001WO-US26519.

XX

XX 25-AUG-2000; 2000US-227948P.

PR

PR 29-AUG-2000; 2000US-228854P.

XX

XX (ILLU-) ILLUMINA INC.

XX

XX Gunderson K;

XX

XX WPI; 2002-292068/33.

XX

XX Array comprising adapter sequences useful for immobilizing or detecting

PT

PT a target nucleic acid sequence, has different addresses comprising

PT

PT different specific capture probes

XX

XX Claim 1; Page 93; 261pp; English.

XX

XX The invention relates to an oligonucleotide array (I) comprising at least

CC

CC 25 different addresses (adapter sequences) with each comprising a

CC

CC different capture probe selected from a group consisting of the sequences

CC

CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target

CC

CC nucleic acid sequence by attaching a adapter nucleic acid

CC

CC nucleic acid sequence to a target nucleic acid to form a modified target

CC

CC nucleic acid and contacting the modified target nucleic acid with (I).

CC

CC The steps of above method is useful for detecting a target nucleic acid,

CC

CC which further comprises detecting the presence of the modified target

CC

CC nucleic acid.

XX

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 other;

Query Match

Best Local Similarity 55.0%; Score 11; DB 24; Length 24;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTCGC 12

Db 11 CAACTCTTCGC 1

RESULT 14

ABQ08101/c

ID ABQ08101 standard; DNA; 24 BP.

XX

AC ABQ08101;

XX

XX 11-JUN-2002 (first entry)

XX

XX Oligonucleotide adapter/capture probe 8092.

XX

XX Oligonucleotide array; adapter sequence; probe; ss.

XX

OS Synthetic.

XX

XX WO200216649-A2.

XX

XX 28-FEB-2002.

XX

XX 27-AUG-2001; 2001WO-US26519.

XX

XX 25-AUG-2000; 2000US-227948P.

PR

PR 29-AUG-2000; 2000US-228854P.

XX

XX (ILLU-) ILLUMINA INC.

XX

XX Gunderson K;

XX

XX WPI; 2002-292068/33.

XX

XX Array comprising adapter sequences useful for immobilizing or detecting

PT

PT a target nucleic acid sequence, has different addresses comprising

PT

PT different specific capture probes

XX

XX Claim 1; Page 189; 261pp; English.

XX

XX The invention relates to an oligonucleotide array (I) comprising at least

CC

CC 25 different addresses (adapter sequences) with each comprising a

CC

CC different capture probe selected from a group consisting of the sequences

CC

CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target

CC

CC nucleic acid sequence by attaching a adapter nucleic acid

CC

CC nucleic acid sequence to a target nucleic acid to form a modified target

CC

CC nucleic acid and contacting the modified target nucleic acid with (I).

CC

CC The steps of above method is useful for detecting a target nucleic acid,

CC

CC which further comprises detecting the presence of the modified target

CC

XX nucleic acid.

XX

SQ Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 other;

Query Match

Best Local Similarity 55.0%; Score 11; DB 24; Length 24;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTCGC 12

Db 11 CAACTCTTCGC 1

XX

RESULT 15

ABQ08142

ID ABQ08142 standard; DNA; 24 BP.

XX

AC ABQ08142;

XX

XX 11-JUN-2002 (first entry)

XX

XX Oligonucleotide adapter/capture probe 8133.

XX

KW Oligonucleotide array; adapter sequence; probe; ss.

PF 28-SEP-1993; 93WO-GB02026.
 XX
 PR 28-SEP-1992; 92GB-0020418.
 XX
 XX (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 XX
 XX Goodenough PW, Gould WM, Moseley BEE, Pickersgill RW;
 PI Varhill K, Gould GW, Moseley BEB, Varvill K;
 XX WPI; 1994-135584/16.
 DR
 XX Preparation of new reduced size polypeptide(s), partic. enzyme(s)
 PT - lacking at least a part of a loop region while retaining
 PT biologically functional activity
 XX
 PS Disclosure; Page 26; 59pp; English.
 XX
 CC This sequence verified a Cys to Thr mutation had occurred
 CC at a position equivalent to codon 94 of a truncated hen egg white
 CC lysozyme gene following site-directed mutagenesis via inverse PCR
 CC using an oligonucleotide
 CC DNA primer (AAQ62039).
 XX
 XX Sequence 21 BP; 8 A; 5 C; 7 G; 1 T; 0 other;
 SQ
 Query Match 55.0%; Score 11; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 TCTTCGGGTG 16
 DB 19 TCTTCGGGTG 9
 RESULT 11
 AAC68689/c
 ID AAC68689 standard; DNA; 22 BP.
 XX
 AC AAC68689;
 XX
 XX 22-FEB-2001 (first entry)
 DT
 XX Mouse R35 specific primer MM-R35-EUL.
 DE
 XX Mouse; R35; uropathic; antiinflammatory; analgesic;
 KW gene therapy; seven transmembrane receptor; neuropathic pain;
 KW inflammation; incontinence; irritable bowel syndrome;
 KW PCR primer; ss.
 XX
 XX Mus musculus.
 OS
 XX WO200064928-A2.
 PN
 XX 02-NOV-2000.
 PD
 XX 20-APR-2000; 2000WO-GB01546.
 PF
 XX 21-APR-1999; 99GB-0009161.
 PR
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA (PLAC) MAX-PLANCK INST NEUROBIOLOGY.
 XX
 XX Barde Y, Friedel R, Michalovich D, Reith AD, Schnuerch H;
 PI Stubbusch J;
 XX WPI; 2000-679669/66.
 DR
 XX Novel R35 polypeptides and polynucleotides useful for treating
 PT neuropathic, inflammatory and chronic pain, incontinence and irritable
 PT bowel syndrome -
 XX
 PS Example 4; Page 25; 55pp; English.

XX The present sequence was used in the cloning of full-length mouse R35
 CC cDNA. R35 is a seven transmembrane receptor which is useful for
 CC treating neuropathic pain, inflammatory and chronic pain, incontinence,
 CC and disorders of the gastrointestinal tract associated with gut motility
 CC and secretion such as irritable bowel syndrome. It is also useful for
 CC inducing an immune response in a mammal to protect against the diseases.
 CC It is useful in screening assays to identify compounds which stimulate or
 CC inhibit the function of the polypeptide, to identify membrane bound or
 CC soluble receptors and also for the structure-based design of an agonist,
 CC antagonist or inhibitor of R35.
 XX
 SQ Sequence 22 BP; 8 A; 5 C; 7 G; 2 T; 0 other;
 Query Match 55.0%; Score 11; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CTCCTTCGGGTG 15
 DB 14 CTCCTTCGGGTG 4
 RESULT 12
 ABK86775
 ID ABK86775 standard; DNA; 22 BP.
 XX
 AC ABK86775;
 XX
 XX 24-SEP-2002 (first entry)
 DT
 XX PCR primer, 28L5, used to amplify 2,5 DKG reductase d (clone pi-28).
 DE
 XX 2,5-diketo-D-gluconic acid reductase d; DKGRd; aldo-keto reductase;
 KW glucose; ascorbic acid; 2-keto-L-gulonic acid; vitamin C; immunogen;
 KW catalytic efficiency; thermal stability; solvent tolerance; pH optimum;
 KW PCR; primer; ss; pi-28.
 XX
 XX Unidentified.
 OS
 XX WO200229019-A2.
 PN
 XX 11-APR-2002.
 PD
 XX 02-OCT-2001; 2001WO-US42445.
 PF
 XX 04-OCT-2000; 2000US-0684385.
 PR
 XX (GEMV) GENENCOR INT INC.
 PA
 XX Donnelly M, Eichenfeldt WH, Trent J;
 PI WPI; 2002-463231/49.
 DR
 XX Diketo-D-gluconic acid reductases, isolated from the environment using
 PT polymerase chain reaction methods, useful to provide new catalysts with
 PT desirable traits for industrial processes -
 XX
 XX Example 1; Page 31; 58pp; English.
 PS
 XX The invention discloses the isolated polypeptide, and polynucleotide
 CC encoding it, 2,5-diketo-D-gluconic acid reductase (DKGR) which is a
 CC member of the aldo-keto reductase superfamily. The reductase, in
 CC particular in Pantoea sp., is useful for converting glucose to ascorbic
 CC acid, by culturing the host cell under conditions suitable for the
 CC expression of DKGR. Glucose is first converted to 2,5-diketo-D-gluconic
 CC acid by endogenous oxidases and this is then reduced enzymatically to
 CC 2-keto-L-gulonic acid by a heterologous DKGR expressed in the production
 CC strain of bacteria. DKGR nucleic acids and proteins are useful to make
 CC enzymes useful in industrial processes to convert glucose to vitamin C in
 CC a single organism. DKGR proteins or their fragments and derivatives are
 CC useful as immunogens to produce antibodies useful in screening for
 CC similar enzymes from other organisms and samples. These antibodies are

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AC AAQ22888;
XX
XX 07-JUL-1992 (first entry)
XX
XX HCV-Hc59 primer #626 (sense strand).
DE
DE Hepatitis C virus; non-A non-B virus; HCV-Hc59; primers;
KW probes; vaccine; ss.
KW
XX Synthetic.
XX
XX WO9203458-A.
XX
XX 05-MAR-1992.
XX
XX 23-AUG-1991; 91WO-US06037.
XX
XX 21-NOV-1990; 90US-0616369.
XX
XX 25-AUG-1990; 90US-0573643.
XX
XX (NYBL-) NEW YORK BLOO DCENT.
XX
XX (PHAA ) PHARMACIA GENETIC ENG INC.
XX
XX Zebedee S, Inchauspe G, Nasofe MS, Prince AM;
XX
XX WPI; 1992-096821/12.
XX
XX Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis
XX virus - obtd. Hutch C59 subgroup encoding polypeptide(s), useful
XX as vaccines, and immuno reactive Abs for diagnosis of virus
XX
XX Disclosure; Page 107; 225pp; English.
XX
XX One Hutch strain (HCV-H) of NANBV, designated the Hutch c59 isolate
XX (HCV-Hc59) was propagated through passage in animals and the
XX entire viral genome was cloned and sequenced.
XX Five microg of purified liver or plasma derived from HCV RNA was
XX used per cDNA priming reaction. Specific nucleotide primers
XX derived from published HCV sequences and spanning the entire
XX reported genomic sequences were used to prime the reaction.
XX Selected target sequences were amplified using a PCR-based approach
XX using a variety of nucleotide primers. The nucleotide sequences
XX of the primers are given in AAQ22872-936 and AAQ24472. Amplified
XX sequences were subsequently isolated, rendered blunt-ended and
XX inserted into a pUC or pBluescript cloning vectors.
XX
XX Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 other;
SQ
Query Match 55.0%; Score 11; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACTCTTCGCGG 14
DB 11 ACTCTTCGCGG 1

RESULT 9
ABL43707/c
ID ABL43707 standard; DNA; 20 BP.
XX
XX ABL43707;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:751.
DE
DE Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
KW genome; PCR primer; ss.
KW
XX Homo sapiens.
XX
XX JP2001321190-A.
XX

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XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-0068285.
XX
XX 10-MAR-2000; 2000JP-0066716.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones -
XX
XX Claim 4; Page 19; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;
SQ
Query Match 55.0%; Score 11; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCCTTCGCGGT 15
DB 15 CTCCTTCGCGGT 5

RESULT 10
AAQ62049/c
ID AAQ62049 standard; DNA; 21 BP.
XX
XX AAQ62049;
XX
XX 09-OCT-1994 (first entry)
XX
XX Hen egg white lysozyme gene Cys to Thr mutation at codon 94.
DE
DE Hen egg white; lysozyme; enzyme engineering; protein engineering
KW fowl; plasmid pKPI500; ss.
KW
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 10..12
XX /*tag= a
XX /note= "Cys to Thr mutation"
XX
XX WO9408018-A.
XX
XX 14-APR-1994.
XX
XX

```


XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABP99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 other;

Query Match 55.0%; Score 11; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTGGC 12
 |||||
 Db 2 CAACTCTTGGC 12

RESULT 6

AAX00290/c
 ID AAX00290 standard; DNA; 13 BP.

XX
 AC AAX00290;

XX 25-MAR-1999 (first entry)

DE Target DNA sequence DNA 6.

XX Melting point; temperature; nucleic acid; fluorescent intensity;
 KW probe; fluorescent intercalative dye; target DNA; diagnosis;
 KW detection; genetic mutation; homology; ss.

XX Synthetic.

XX EP892071-A2.

XX 20-JAN-1999.

XX 05-JUN-1998; 98EP-0304458.

XX 05-JUN-1997; 97JP-0147825.

XX (TOYU) TOSOH CORP.

XX Ishiguro T, Saitoh J;

XX WPI; 1999-083587/08.

XX Measuring melting temperature of nucleic acid - comprises monitoring
 PT fluorescent intensity of mixture of sample and fluorescently
 PT labelled probe

PS Example 3; Page 7; 24pp; English.

XX A method has been developed of measuring the melting temperature of a
 CC nucleic acid. The method comprises monitoring the fluorescent intensity
 CC of a mixture of a sample and a probe labelled with a fluorescent
 CC intercalative dye at different temperatures. The probe contains a base
 CC sequence complementary to a specific nucleic acid in the sample. The
 CC method is useful for clinical gene diagnosis by exploring unknown genes.
 CC It is useful for evaluating the homology of an unknown gene with a
 CC control gene sequence and as a method of detecting genetic mutations
 CC e.g. therapy for hepatitis C virus (HCV). The method is quicker and
 CC requires less labour as it specifically detects and quantifies the
 CC hybrid in a simple one-step measurement without requiring the separation
 CC of excess unhybridised probe. The method is more sensitive and can

CC detect small amounts of nucleic acids in sample e.g. tens of copies of
 CC target nucleic acids can be amplified to several ng. The present
 CC sequence represents a target DNA sequence from an example of the present
 CC invention.

XX Sequence 13 BP; 2 A; 5 C; 5 G; 1 T; 0 other;

Query Match 55.0%; Score 11; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCGCGTGGCA 19
 |||||
 Db 12 TCGCGTGGCA 2

RESULT 7

AAQ06516/c
 ID AAQ06516 standard; DNA; 20 BP.

XX
 AC AAQ06516;

XX 22-FEB-1991 (first entry)

XX Probe/primer TB-5 derived from mycobacterial gene.

XX mycobacterial antigen; actinomycetales; tuberculosis; ss.

XX Synthetic.

XX WO9012875-A.

XX 01-NOV-1990.

XX 13-APR-1990; 90WO-FR00274.

XX 17-APR-1989; 89FR-0005057.

XX (INRM) INSERM INST NAT SANTE.

XX (INSP) INST PASTEUR.

XX Hance A, Grandchamp-Desraux B, Levy-Frebault V, Gicouel B;

XX WPI; 1990-348478/46.

XX Nucleotide sequences of actinomycetales - used as primers for
 PT synthesis of DNA of actinomycetales

XX Claim 24; Page 39; 61pp; French.

XX This sequence is based on a fragment of a mycobacterial gene which
 CC encodes a protein homologous to the 65KD antigen of mycobacterium.
 CC TB-5 is used in a pair as a primer to amplify
 CC mycobacterial genes to detect mycobacteria. The oligonucleotide can
 CC also be used as a labelled probe to detect amplified mycobacterial
 CC sequences. It reacts specifically with Mycobacterium avium DNA.
 CC See also AAQ06505-Q06515, AAQ06517-Q06523 and AAR08336.

XX Sequence 20 BP; 2 A; 11 C; 4 G; 3 T; 0 other;

Query Match 55.0%; Score 11; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
 |||||
 Db 11 CGCGGTGGCAG 1

RESULT 8

AAQ22888/c
 ID AAQ22888 standard; DNA; 20 BP.

XX

XX PI Cosman DJ, Dower SK, Lupton SD, Mosley BA, Sims JB;
 XX DR WPI; 1998-361746/31.
 XX PT Regulation of interleukin-1 mediated immune or inflammatory response
 XX PT in mammal - comprises administering soluble IL-1 receptor protein,
 XX PT used in treatment of e.g. graft versus host disease and multiple
 XX PT sclerosis
 XX PS Example 1; Column 19; 33pp; English.
 XX CC AAV34748-V34756 are primers used in the isolation of human and mouse
 XX CC type II interleukin-1 receptor (IL-1R) which is used in a method to
 XX CC investigate the regulation of the immune or inflammatory response in a
 XX CC mammal. This method involves administering a soluble type-II IL-1
 XX CC receptor protein in an amount effective to bind to IL-1 and prevent its
 XX CC binding to cell-surface IL-1 receptors. The process can be used for
 XX CC treating alloantigen-induced rejection of transplanted tissues or
 XX CC organs, graft-versus-host disease and autoimmune dysfunction dependent
 XX CC upon the activation of T cells against self antigens, selected from
 XX CC rheumatoid arthritis, diabetes mellitus or multiple sclerosis.
 XX SQ Sequence 46 BP; 6 A; 12 C; 14 G; 14 T; 0 other;
 Query Match 65.0%; Score 13; DB 19; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0;
 QY 3 AACTCTTCGCGGT 15
 DB 25 AACTCTTCGCGGT 37
 RESULT 4
 AAF80328 ID AAF80328 standard; DNA; 26 BP.
 AC AAF80328;
 XX 29-JUN-2001 (first entry)
 XX PCR primer for cDNA encoding the G-protein coupled receptor IGS4.
 XX Human; G-protein coupled receptor; IGS4; IGS4A; schizophrenia;
 XX nervous system disorder; psychiatric disorder; Parkinson's disease;
 XX episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke;
 XX cardiovascular disease; heart failure; angina pectoris; obesity; emesis;
 XX motility disorder; myocardial infarction; hypertension; dyslipidemia;
 XX gastrointestinal disorder; inflammatory bowel disease; osteoporosis;
 XX inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
 XX gynecological disorder; PCR primer; ss.
 XX OS Homo sapiens.
 XX WO200125269-A2.
 XX 12-APR-2001.
 XX 25-SEP-2000; 2000WO-EP09584.
 XX 24-SEP-1999; 99EP-0203140.
 XX 28-JUL-2000; 99NL-1013140.
 XX 31-JUL-2000; 2000EP-0202683.
 XX (SOLV) SOLVAY PHARM BV.
 XX Deleersnijder W, Berger C, Loeken C, Nys G, Venema J;
 XX WPI; 2001-273568/28.
 XX New G-protein coupled receptors and the polynucleotides encoding them,

PT useful for preventing, ameliorating or correcting nervous system
 PT disorders, cardiovascular diseases, dyslipidemias, inflammations, pain
 PT or cancers
 XX Example 1a; Page 39; 102pp; English.
 XX PCR primers AAF80328-30 were used to amplify cDNA encoding a
 XX human G-protein coupled receptor designated IGS4. IGS4 exists in two
 XX polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4
 XX polynucleotides are useful for preventing, ameliorating or correcting
 XX dysfunctions or diseases. These diseases include peripheral nervous
 XX system, psychiatric and central nervous system disorders
 XX (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's
 XX disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases
 XX (e.g. heart failure, angina pectoris, myocardial infarction or
 XX hypertension), dyslipidemias, obesity, emesis, gastrointestinal
 XX disorders (e.g. inflammatory bowel disease or motility disorders),
 XX osteoporosis, inflammations, infections (e.g. bacterial, fungal,
 XX protozoan or viral), pain, cancers, immune disorders, allergies,
 XX sepsis or gynecological disorders. Agonists or antagonists of IGS4 are
 XX effective with regard to disorders of the nervous system, including the
 XX central and peripheral nervous systems, disorders of the gastrointestinal
 XX system, cardiovascular system, skeletal muscle, thyroid, lung or
 XX genitourinary system, or immunological disease. The IGS4 polynucleotides
 XX are useful as diagnostic reagents for detecting under-expression,
 XX overexpression or altered expression of IGS4.
 XX SQ Sequence 26 BP; 1 A; 7 C; 9 G; 5 T; 4 other;
 Query Match 60.0%; Score 12; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02; Mismatches 0; Gaps 0;
 Matches 12; Conservative 0; Indels 0;
 QY 6 TCTTCGCGGTGG 17
 DB 5 TCTTCGCGGTGG 16
 RESULT 5
 ABI41062 ID ABI41062 standard; DNA; 12 BP.
 XX ABI41062;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 341035 for detecting SNP TSC0010735.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status
 XX Claim 1; SEQ ID 341035; 29pp + Sequence Listing; German.
 PS

```

XX  New polynucleotide(s) anti:sense to human telomerase - used for
PT  detecting or inhibiting human telomerase, e.g. for treating cancers,
PT  contraception, immuno-suppression or treating infection
XX  Claim 11; Page 65; 80pp; English.
XX  Sequences shown in AAV41169 to AAV41181 represent antisense
CC  oligonucleotides to the RNA component of human telomerase (hTR). These
CC  antisense oligonucleotides specifically hybridise to a nucleotide
CC  sequence within an accessible region of the hTR, but that does not
CC  hybridise to a sequence within the template region of hTR. These
CC  oligonucleotides may specifically be used for detection of an RNA
CC  component of human telomerase in a sample. This is useful for diagnosing
CC  cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC  and providing prognosis for a cancer patient. The inhibitory
CC  oligonucleotides can inhibit the telomerase activity level in a cell by
CC  interfering with transcription of the RNA component, decreasing the
CC  half-life of the telomerase RNA component transcript, inhibiting assembly
CC  of the RNA component into the telomerase holoenzyme, or inhibiting the
CC  polymerase activity of telomerase. These antisense oligonucleotides can
CC  be used for inhibiting telomerase activity in both cultured cells and in
CC  cells in vivo. They can be used in therapeutics for treating or
CC  preventing cancer, for contraception or sterilisation, for
CC  immunosuppression, and for selectively down-regulating specific branches
CC  of the immune system, e.g. a specific subset of T-cells, in
CC  anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC  parasites or fungi.
XX  Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;
SQ  Query Match 100.0%; Score 20; DB 19; Length 20;
    Best Local Similarity 100.0%; Pred. No. 0.012;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CCAACTCTTCGGGTGGCAG 20
    |||||
Db  1 CCAACTCTTCGGGTGGCAG 20

RESULT 2
AAV41172
ID  AAV41172 standard; DNA; 30 BP.
XX
AC  AAV41172;
XX
DT  08-OCT-1998 (first entry)
XX
DE  RNA component of human telomerase (hTR) antisense oligo 16.
XX
KW  RNA component; human telomerase; antisense oligonucleotide; infection;
KW  neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW  contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW  immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
FN  W09828442-A1.
XX
PD  02-JUL-1998.
XX
PF  19-DEC-1997; 97WO-US23619.
XX
PR  20-DEC-1996; 96US-0770565.
PR  20-DEC-1996; 96US-0770564.
XX
PA  (GERO-) GERON CORP.
XX
PI  Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX  WPI; 1998-377670/32.
XX

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PT  New polynucleotide(s) anti:sense to human telomerase - used for
PT  detecting or inhibiting human telomerase, e.g. for treating cancers,
PT  contraception, immuno-suppression or treating infection
XX  Claim 11; Page 65; 80pp; English.
XX  Sequences shown in AAV41169 to AAV41181 represent antisense
CC  oligonucleotides to the RNA component of human telomerase (hTR). These
CC  antisense oligonucleotides specifically hybridise to a nucleotide
CC  sequence within an accessible region of the hTR, but that does not
CC  hybridise to a sequence within the template region of hTR. These
CC  oligonucleotides may specifically be used for detection of an RNA
CC  component of human telomerase in a sample. This is useful for diagnosing
CC  cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC  and providing prognosis for a cancer patient. The inhibitory
CC  oligonucleotides can inhibit the telomerase activity level in a cell by
CC  interfering with transcription of the RNA component, decreasing the
CC  half-life of the telomerase RNA component transcript, inhibiting assembly
CC  of the RNA component into the telomerase holoenzyme, or inhibiting the
CC  polymerase activity of telomerase. These antisense oligonucleotides can
CC  be used for inhibiting telomerase activity in both cultured cells and in
CC  cells in vivo. They can be used in therapeutics for treating or
CC  preventing cancer, for contraception or sterilisation, for
CC  immunosuppression, and for selectively down-regulating specific branches
CC  of the immune system, e.g. a specific subset of T-cells, in
CC  anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC  parasites or fungi.
XX  Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ  Query Match 100.0%; Score 20; DB 19; Length 30;
    Best Local Similarity 100.0%; Pred. No. 0.012;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CCAACTCTTCGGGTGGCAG 20
    |||||
Db  11 CCAACTCTTCGGGTGGCAG 30

RESULT 3
AAV34750
ID  AAV34750 standard; DNA; 46 BP.
XX
AC  AAV34750;
XX
DT  27-AUG-1998 (first entry)
XX
DE  Human Type II IL-1R primer #3.
XX
KW  Type II interleukin-1 receptor; IL-1R; immune response; inflammation;
KW  regulation; soluble; cell surface receptor; treatment; alloantigen;
KW  tissue; organ; rejection; transplant; graft-versus-host disease; human;
KW  autoimmune dysfunction; T-cell activation; self antigen; primer;
KW  rheumatoid arthritis; diabetes mellitus; multiple sclerosis; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
FN  US5767064-A.
XX
PD  16-JUN-1998.
XX
PF  16-MAY-1995; 95US-0442043.
XX
PR  16-MAY-1991; 91US-0701415.
PR  05-JUN-1990; 90US-0534193.
PR  24-AUG-1990; 90US-0573576.
PR  13-DEC-1990; 90US-0627071.
PR  12-JUL-1993; 93US-0091519.
PR  13-MAY-1994; 94US-0242211.
PR  16-MAY-1995; 95US-0442043.
XX
PA  (IMV ) IMMUNEX CORP.
XX

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20

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Scoring table: OLIGO_NUC

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Searched: 2185239 seqs, 112599159 residues

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- 21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	20	100.0	20	19	AAV41174		RNA component of h
2	20	100.0	30	19	AAV41172		Human component of h
3	13	65.0	46	19	AAV4750		Human Type II IL-1
4	12	60.0	26	22	AAF80328		PCR primer for CDN
5	11	55.0	12	23	AB141062		Oligonucleotide pr
6	11	55.0	13	20	AAK00290		Target DNA sequenc
7	11	55.0	20	11	AAQ06516		Probe/primer TB-5
8	11	55.0	20	13	AAQ22888		HCV-Hc5 primer #6
9	11	55.0	20	24	ABL43707		Human chromosome 1

c	10	55.0	21	15	AAQ62049	Hen egg white lyso
c	11	55.0	22	21	ABC68689	Mouse R35 specific
c	12	55.0	22	24	ABK67775	PCR primer, 28L5,
c	13	55.0	24	24	ABQ02087	Oligonucleotide ad
c	14	55.0	24	24	ABQ08101	Oligonucleotide ad
c	15	55.0	24	24	ABQ08142	Oligonucleotide ad
c	16	55.0	22	22	AAH37711	SNP specific SNPE
c	17	55.0	28	20	AAZ29951	PCR primer DYV-218
c	18	55.0	36	22	AAH15371	Oligo 5R, to const
c	19	55.0	36	22	AAH84898	Human SEC2 DNA amp
c	20	55.0	37	19	AAV24106	Primer for T7 gene
c	21	55.0	48	22	AAH67727	Murine insulin-like
c	22	55.0	48	22	AAH67731	Rat insulin-like g
c	23	55.0	10	22	AAF40580	Yeast NORF gene SA
c	24	50.0	10	22	AB119475	Oligonucleotide pr
c	25	50.0	12	23	AB142091	Oligonucleotide pr
c	26	50.0	12	23	AB154849	Oligonucleotide pr
c	27	50.0	12	23	AB181242	Oligonucleotide pr
c	28	50.0	13	23	ABC17514	Oligonucleotide SE
c	29	50.0	13	23	ABC70350	Oligonucleotide SE
c	30	50.0	13	23	ABC70351	Oligonucleotide SE
c	31	50.0	13	23	ABC70351	Oligonucleotide SE
c	32	50.0	13	23	ABF47778	Oligonucleotide SE
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c	34	50.0	13	23	ABF97740	Oligonucleotide SE
c	35	50.0	13	23	ABH33140	Oligonucleotide SE
c	36	50.0	13	23	ABH33141	Oligonucleotide SE
c	37	50.0	13	23	ABH33141	Oligonucleotide SE
c	38	50.0	15	16	AAH52289	Mouse ICAM hammerh
c	39	50.0	18	12	AAQ13542	Probe JFL330 to co
c	40	50.0	18	17	AAH71901	Primer for detecti
c	41	50.0	18	17	AAH71901	Primer for detecti
c	42	50.0	18	19	AAV08260	PCR primer ABCR, EX
c	43	50.0	18	21	AAA30862	Fragment of a plas
c	44	50.0	18	24	ABK41162	Human obesity-asso
c	45	50.0	19	19	AAV46209	Human HLA-A primer

ALIGNMENTS

RESULT 1

AAV41174

ID AAV41174 standard; DNA; 20 BP.

XX AAV41174;

XX 08-OCT-1998 (first entry)

DT RNA component of human telomerase (hTR) antisense oligo 16bc.

DE RNA component; human telomerase; antisense oligonucleotide; infection;

XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;

KW contraception; sterilisation; immunosuppression; therapeutic; hTR;

KW immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

XX 02-JUL-1998.

XX 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

XX 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

DR

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OM nucleic - nucleic search, using sw model

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(without alignments)
195.867 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	30	2	US-08-770-565-5
3	14	70.0	45	6	5198342-4
4	13	65.0	46	1	US-08-091-519-5
5	13	65.0	46	1	US-08-106-507-7
6	13	65.0	46	1	US-08-442-043A-5
7	13	65.0	46	5	PCT-US91-03478-5
8	11	55.0	20	2	US-08-473-020A-13
9	11	55.0	30	1	US-08-495-743-60
10	11	55.0	30	1	US-08-495-739-60
11	11	55.0	30	1	US-08-495-741-60
12	11	55.0	30	4	US-08-062-023-60
13	11	55.0	38	1	US-08-664-449-61
14	10	50.0	11	1	US-07-778-233B-3
15	10	50.0	11	1	US-07-963-321-3
16	10	50.0	11	1	US-08-290-641-3
17	10	50.0	11	1	US-08-548-540-3
18	10	50.0	11	5	PCT-US96-09809-3
19	10	50.0	15	2	US-08-232-620A-451
20	10	50.0	15	3	US-09-071-845-451
21	10	50.0	18	1	US-08-599-252-1
22	10	50.0	18	1	US-08-436-074-1
23	10	50.0	18	5	PCT-US96-06352-1
24	10	50.0	18	5	PCT-US96-06583-1
25	10	50.0	20	2	US-08-770-565-6
26	10	50.0	20	2	US-08-578-551-10
27	10	50.0	20	2	US-08-473-020A-14

c	28	10	50.0	20	2	US-09-289-368-52	Sequence 52, Appl
c	29	10	50.0	20	2	US-09-190-982-10	Sequence 10, Appl
c	30	10	50.0	20	4	US-09-408-257-10	Sequence 10, Appl
c	31	10	50.0	20	4	US-09-136-411-7	Sequence 7, Appl
c	32	10	50.0	20	4	US-09-472-035A-12	Sequence 12, Appl
c	33	10	50.0	20	4	US-09-545-686-26	Sequence 26, Appl
c	34	10	50.0	20	4	US-09-291-541-5	Sequence 5, Appl
c	35	10	50.0	21	4	US-09-338-907-420	Sequence 420, App
c	36	10	50.0	21	4	US-09-218-207-420	Sequence 420, App
c	37	10	50.0	21	4	US-09-291-541-2	Sequence 2, Appl
c	38	10	50.0	24	1	US-08-203-905B-25	Sequence 25, Appl
c	39	10	50.0	26	1	US-08-318-193-28	Sequence 28, Appl
c	40	10	50.0	26	1	US-08-318-193-29	Sequence 29, Appl
c	41	10	50.0	26	4	US-09-224-426-5	Sequence 5, Appl
c	42	10	50.0	26	4	US-09-478-601-5	Sequence 5, Appl
c	43	10	50.0	26	4	US-09-478-602-5	Sequence 5, Appl
c	44	10	50.0	28	1	US-07-844-297-5	Sequence 5, Appl
c	45	10	50.0	28	1	US-07-681-703B-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-7

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACTCTTCGGCGTGCAG 20

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAACTCTTCGGGT 15
| | | | | | | | | | | | | | | | | |
Db 23 CAACTCTTCGGGT 36

RESULT 4
US-08-091-519-5
; Sequence 5, Application US/08091519
; Patent No. 5350683
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/701,415
; FILING DATE:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: N
; ANTI-SENSE: N
; US-08-091-519-5

Query Match 65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 AACTTTCGGGT 15
| | | | | | | | | | | | | | | | | |
Db 25 AACTTTCGGGT 37

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGGGTGGCAG 20
| | | | | | | | | | | | | | | | | |
Db 11 CCAACTCTTCGGGTGGCAG 30

RESULT 3
US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Puzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-5

Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAACTCTTCGGGTGGCAG 20
| | | | | | | | | | | | | | | | | |
Db 11 CCAACTCTTCGGGTGGCAG 30

Query Match 70.0%; Score 14; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-08-106-507-7
; Sequence 7, Application US/08106507
; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,507
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,648
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: oligonucleotide
US-08-106-507-7

Query Match 65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGT 15
Db 25 AACTCTTCGGGT 37

RESULT 6
US-08-442-043A-5
; Sequence 5, Application US/08442043A
; Patent No. 5767064
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,043A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-442-043A-5

Query Match 65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGT 15
Db 25 AACTCTTCGGGT 37

RESULT 7
PCT-US91-03478-5
; Sequence 5, Application PC/TUS9103478
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

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STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US91/03478
  FILING DATE: 19910517
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/534,193
    FILING DATE: 06-JUN-1990
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/573,576
    FILING DATE: 24-AUG-1990
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/627,071
    FILING DATE: 13-DEC-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: Wight, Christopher L.
    REGISTRATION NUMBER: 31680
    REFERENCE/DOCKET NUMBER: 2003-WO
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 206-587-5570
      TELEFAX: 206-233-0644
  INFORMATION FOR SEQ ID NO: 5:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 46 base pairs
      TYPE: NUCLEIC ACID
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: DNA (genomic)
      HYPOTHETICAL: N
      ANTI-SENSE: N
PCT-US91-03478-5

Query Match 65.0%; Score 13; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACCTTCGCGGT 15
   |||||
Db 25 AACCTTCGCGGT 37

RESULT 8
US-08-473-020A-13/c
; Sequence 13, Application US/08473020A
; Patent No. 5877273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desaux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Gicquel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; applications to the synthesis or detection of nucleic
; acids, products of expression of such sequences and
; application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/473,020A
  FILING DATE: 06-JUN-1995
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/623,729
    FILING DATE: 14-DEC-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: Dreger, Walter H
    REGISTRATION NUMBER: 24190
    REFERENCE/DOCKET NUMBER: A54435
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 781-1989
      TELEFAX: (415) 398-3249
  INFORMATION FOR SEQ ID NO: 13:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 20 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: CDNA
US-08-473-020A-13

Query Match 55.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
   |||||
Db 11 CGCGGTGGCAG 1

RESULT 9
US-08-495-743-60/c
; Sequence 60, Application US/08495743
; Patent No. 5654416
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Cummins, Susan M. Atwood
; APPLICANT: Lynn Bergmeyer, John B. Findlay
; APPLICANT: John W.H. Sutherland, JoAnne H. Kerschner
; TITLE OF INVENTION: DIAGNOSTIC COMPOSITIONS, ELEMENTS,
; METHODS AND TEST KITS FOR
; TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF TWO
; OR MORE TARGET DNA'S USING PRIMERS
; TITLE OF INVENTION: HAVING MATCHED MELTING TEMPERATURES
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Kodak Company, Patent Legal Staff
; STREET: 343 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14650 - 2201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44 MB storage (IBM)
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: PC-8 (Word for Windows)
; CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/495,743
  FILING DATE: 08-JUN-1995
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/062,023
    FILING DATE: 14-MAY-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Tucker, J. Lanny
    REGISTRATION NUMBER: 27,678
    REFERENCE/DOCKET NUMBER: 67271A
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (716) 722-9332
      TELEFAX: (716) 477-4646
```


INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Probe for Mycobacterium
MOLECULE TYPE: avium DNA
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE: Synthetically prepared
IMMEDIATE SOURCE: Same
PUBLICATION INFORMATION: Unknown
US-08-495-743-60

Query Match 55.0%; Score 11; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
||| |||||
Db 21 CGCGGTGGCAG 11

RESULT 10

US-08-495-739-60/c
Sequence 60, Application US/08495739
Patent No. 5702901
GENERAL INFORMATION:
APPLICANT: Thomas J. Cummins, Susan M. Atwood
APPLICANT: Lynn Bergmeyer, John B. Findlay
APPLICANT: John W.H. Sutherland, JoAnne H. Kerschner
TITLE OF INVENTION: DIAGNOSTIC COMPOSITIONS, ELEMENTS,
TITLE OF INVENTION: METHODS AND TEST KITS FOR
TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF TWO
TITLE OF INVENTION: OR MORE TARGET DNA'S USING PRIMERS
TITLE OF INVENTION: HAVING MATCHED MELTING TEMPERATURES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Kodak Company, Patent Legal Staff
STREET: 343 State Street
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14650 - 2201
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44 MB storage (IBM)
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: PC-8 (Word for Windows)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,739
FILING DATE: 08-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US/08/062,023
FILING DATE: 14 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: Tucker, J. Lanny
REGISTRATION NUMBER: 27,678
REFERENCE/DOCKET NUMBER: 67271A
TELEPHONE: (716) 722-9332
TELEFAX: (716) 477-4646
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Probe for Mycobacterium
MOLECULE TYPE: avium DNA
HYPOTHETICAL: No

ANTI-SENSE: No
ORIGINAL SOURCE: Synthetically prepared
IMMEDIATE SOURCE: Same
PUBLICATION INFORMATION: Unknown
US-08-495-739-60

Query Match 55.0%; Score 11; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCAG 20
||| |||||
Db 21 CGCGGTGGCAG 11

RESULT 11

US-08-495-741-60/c
Sequence 60, Application US/08495741
Patent No. 5733751
GENERAL INFORMATION:
APPLICANT: Thomas J. Cummins, Susan M. Atwood
APPLICANT: Lynn Bergmeyer, John B. Findlay
APPLICANT: John W.H. Sutherland, JoAnne H. Kerschner
TITLE OF INVENTION: DIAGNOSTIC COMPOSITIONS, ELEMENTS,
TITLE OF INVENTION: METHODS AND TEST KITS FOR
TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF TWO
TITLE OF INVENTION: OR MORE TARGET DNA'S USING PRIMERS
TITLE OF INVENTION: HAVING MATCHED MELTING TEMPERATURES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Kodak Company, Patent Legal Staff
STREET: 343 State Street
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14650 - 2201
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44 MB storage (IBM)
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: PC-8 (Word for Windows)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,741
FILING DATE: 08-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US/08/062,023
FILING DATE: 19930514
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tucker, J. Lanny
REGISTRATION NUMBER: 27,678
REFERENCE/DOCKET NUMBER: 67271A
TELEPHONE: (716) 722-9332
TELEFAX: (716) 477-4646
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Probe for Mycobacterium
MOLECULE TYPE: avium DNA
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE: Synthetically prepared
IMMEDIATE SOURCE: Same
PUBLICATION INFORMATION: Unknown
US-08-495-741-60

Query Match 55.0%; Score 11; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;

US-18-664-449-61/C

FILING DATE: 199111016

FILING DATE: 19911016

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-778-233B-3

Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCA 19
|||||
Db 10 CGCGGTGGCA 1

RESULT 15

US-07-963-321-3/c
Sequence 3, Application US/07963321
Patent No. 538665
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,321
FILING DATE: 19921015
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,223
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50-1
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-963-321-3

Query Match 50.0%; Score 10; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGGCA 19
|||||
Db 10 CGCGGTGGCA 1

Search completed: June 23, 2003, 10:17:06
Job time : 32.3147 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGGCAG 20

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Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	65.0	46	9	US-10-199-209-5
2	12	60.0	25	9	US-10-098-2638-31566
3	11	55.0	24	9	US-09-940-185-2094
4	11	55.0	25	9	US-10-098-2638-97446
5	11	55.0	25	9	US-10-098-2638-110352
6	11	55.0	25	9	US-10-098-2638-129624
7	11	55.0	36	8	US-08-961-888-12
8	11	55.0	36	9	US-10-002-050-29
9	11	55.0	36	9	US-10-002-304-29
10	11	55.0	36	12	US-10-003-152-29
11	10	50.0	20	9	US-09-971-894-12
12	10	50.0	20	10	US-09-909-849-17
13	10	50.0	21	9	US-09-853-526-420
14	10	50.0	21	10	US-09-901-484A-420
15	10	50.0	22	9	US-09-487-318-11
16	10	50.0	22	10	US-09-930-251-16
17	10	50.0	22	10	US-09-930-251-17
18	10	50.0	22	10	US-09-930-251-18
19	10	50.0	24	12	US-10-077-894-20

20	10	50.0	25	9	US-10-215-112-11414	Sequence 11414, A
21	10	50.0	25	9	US-10-098-2638-26951	Sequence 26951, A
22	10	50.0	25	9	US-10-098-2638-42033	Sequence 42033, A
23	10	50.0	25	9	US-10-098-2638-42034	Sequence 42034, A
24	10	50.0	25	9	US-10-098-2638-72819	Sequence 72819, A
25	10	50.0	25	9	US-10-098-2638-89453	Sequence 89453, A
26	10	50.0	25	9	US-10-098-2638-89454	Sequence 89454, A
27	10	50.0	25	9	US-10-098-2638-95961	Sequence 95961, A
28	10	50.0	25	9	US-10-098-2638-97445	Sequence 97445, A
29	10	50.0	25	9	US-10-098-2638-98053	Sequence 98053, A
30	10	50.0	25	9	US-10-098-2638-98054	Sequence 98054, A
31	10	50.0	25	9	US-10-098-2638-99917	Sequence 99917, A
32	10	50.0	25	9	US-10-098-2638-106052	Sequence 106052, A
33	10	50.0	25	9	US-10-098-2638-108811	Sequence 108811, A
34	10	50.0	25	9	US-10-098-2638-118620	Sequence 118620, A
35	10	50.0	25	9	US-10-098-2638-130018	Sequence 130018, A
36	10	50.0	26	9	US-10-029-314-5	Sequence 5, Appli
37	10	50.0	26	9	US-09-899-732-5	Sequence 5, Appli
38	10	50.0	26	10	US-09-118-276-16	Sequence 16, Appli
39	10	50.0	26	10	US-09-885-478-5	Sequence 5, Appli
40	10	50.0	27	10	US-09-824-984-9	Sequence 9, Appli
41	10	50.0	27	10	US-09-824-851-9	Sequence 9, Appli
42	10	50.0	27	10	US-09-825-247A-9	Sequence 9, Appli
43	10	50.0	27	10	US-09-824-905A-9	Sequence 9, Appli
44	10	50.0	27	10	US-09-825-246A-9	Sequence 9, Appli
45	10	50.0	27	10	US-09-825-245-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-10-199-209-5

; Sequence 5, Application US/10199209

; Publication No. US20030060616A1

; GENERAL INFORMATION:

; APPLICANT: Sims, John E.

; Cosman, David J.

; Lupton, Stephen D.

; Mosley, Bruce A.

; Dower, Steven K.

; TITLE OF INVENTION: Type II Interleukin-1 Receptors

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/199,209

; FILING DATE: 19-Jul-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/461,908

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/08/091,519

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/07/701,415

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 07/534,193

; FILING DATE: 06-JUN-1990

; APPLICATION NUMBER: US 07/573,576

; FILING DATE: 24-AUG-1990

; APPLICATION NUMBER: US 07/627,071

; FILING DATE: 13-DEC-1990

; ATTORNEY/AGENT INFORMATION:

```
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5
    Query Match      65.0%; Score 13; DB 9; Length 46;
    Best Local Similarity 100.0%; Pred. No. 81;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 AACTCTTCGCGGT 15
      |||||
Db      25 AACTCTTCGCGGT 37

RESULT 2
US-10-098-263B-31566
; Sequence 31566, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-31566
    Query Match      60.0%; Score 12; DB 9; Length 25;
    Best Local Similarity 100.0%; Pred. No. 3.5e+02;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TCTTCGCGGTGG 17
      |||||
Db      5 TCTTCGCGGTGG 16

RESULT 3
US-09-940-185-2094/c
; Sequence 2094, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 2094
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2094
    Query Match      55.0%; Score 11; DB 9; Length 24;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCAACTCTTCGC 12
      |||||
Db      11 CCAACTCTTCGC 1

RESULT 4
US-10-098-263B-97446
; Sequence 97446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 97446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-97446
    Query Match      55.0%; Score 11; DB 9; Length 25;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CTCTTCGCGGT 15
      |||||
Db      3 CTCTTCGCGGT 13

RESULT 5
US-10-098-263B-110352
; Sequence 110352, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110352
    Query Match      55.0%; Score 11; DB 9; Length 25;
    Best Local Similarity 100.0%; Pred. No. 1.4e+03;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCAACTCTTCG 11
      |||||
Db      4 CCAACTCTTCG 14
```

RESULT 6

US-10-098-263B-129624
; Sequence 129624, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-129624

Query Match 55.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCG 11
|||||
DB 9 CCAACTCTTCG 19

RESULT 7

US-08-961-888-12
; Sequence 12, Application US/08961888
; Patent No. US20010016351A1
; GENERAL INFORMATION:

; APPLICANT: Padgett, Kerstien
; TITLE OF INVENTION: Sorage, Joseph
; TITLE OF INVENTION: No. US20010016351A1 Vector For Gene Expression
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,888
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I
; REGISTRATION NUMBER: 32,660
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-7451
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
US-08-961-888-12

Query Match 55.0%; Score 11; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCCTCGCGGT 15
|||||
DB 11 CTCCTCGCGGT 21

RESULT 8

US-10-002-050-29
; Sequence 29, Application US/10002050
; Publication No. US20030032095A1
; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Sem
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Chemically
; OTHER INFORMATION: synthesized

US-10-002-050-29

Query Match 55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCGGTGCAG 20
|||||
DB 20 CGCGGTGCAG 30

RESULT 9

US-10-002-304-29
; Sequence 29, Application US/10002304
; Publication No. US20030036185A1
; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-58
; CURRENT APPLICATION NUMBER: US/10/002,304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

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; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically
; OTHER INFORMATION: synthesized
US-10-002-304-29

Query Match          55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
    |||||
Db 20 CGCGGTGGCAG 30

RESULT 10
US-10-003-152-29
; Sequence 29, Application US/10003152
; Patent No. US20020151494A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: No. US20020151494A1e1 Amino Acid Sequences for Human Semaphorin-1
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003.152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically
; OTHER INFORMATION: synthesized
US-10-003-152-29

Query Match          55.0%; Score 11; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
    |||||
Db 20 CGCGGTGGCAG 30

RESULT 11
US-09-971-894-12/c
; Sequence 12, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kashi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Eitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerstein, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR PROKARYOTE CLASSIFICAT
; FILE REFERENCE: 01/22569
; CURRENT APPLICATION NUMBER: US/09/971,894
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
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; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-971-894-12

Query Match          50.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGCGGT 15
    |||||
Db 11 TCTTCGCGGT 2

RESULT 12
US-09-909-849-17
; Sequence 17, Application US/09909849
; Patent No. US20020106754A1
; GENERAL INFORMATION:
; APPLICANT: Tauch, Andreas
; TITLE OF INVENTION: Nucleotide Sequences Which Code for the alr Gene
; FILE REFERENCE: 032301 WD 173
; CURRENT APPLICATION NUMBER: US/09/909,849
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-909-849-17

Query Match          50.0%; Score 10; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCGGTGGCAG 20
    |||||
Db 11 GCGGTGGCAG 20

RESULT 13
US-09-853-526-420
; Sequence 420, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 420
; LENGTH: 21
; TYPE: DNA
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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer for SEQ 257, SEQ 334
US-09-853-526-420

Query Match      50.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCAACTCTTC 10
        |||||
Db       12 CCAACTCTTC 21

RESULT 14
US-09-901-484A-420
; Sequence 420, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T11XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 420
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: downstream amplification primer for SEQ 257, SEQ 334
US-09-901-484A-420

Query Match      50.0%; Score 10; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCAACTCTTC 10
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Db       12 CCAACTCTTC 21

RESULT 15
US-09-487-318-11/c
; Sequence 11, Application US/09487318
; Publication No. US20020182188A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Lola M
; APPLICANT: Nicholas, Moss
; APPLICANT: Hiroshi, Kubota
; TITLE OF INVENTION: Human Liver Progenitors
; FILE REFERENCE: 212875-00101
; CURRENT APPLICATION NUMBER: US/09/487,318
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/116,331
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; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-487-318-11

Query Match      50.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CCAACTCTTCG 11
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Db       22 CCAACTCTTCG 13

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20

Sequence: 1 CCAACTCTTCGCGGTGGCAG 20

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Gapop 60.0 , Gapext 60.0

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35: /cgn2_6/ptodata/2/pna/US099B COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	30	1	PCT-US97-23619-5 Sequence 5, Appli
4	20	100.0	30	11	US-08-770-564A-5 Sequence 5, Appli
C 5	18	90.0	25	36	US-09-956-604A-105231 Sequence 105231,
C 6	18	90.0	25	36	US-09-956-604A-105231 Sequence 105231,
C 7	18	90.0	25	36	US-09-956-604B-105231 Sequence 105231,
C 8	18	90.0	25	67	US-60-234-049-86453 Sequence 86453, A
C 9	16	80.0	24	9	US-08-521-634-15 Sequence 15, Appli
10	13	65.0	46	3	US-07-941-648-7 Sequence 7, Appli
11	13	65.0	46	8	US-08-441-893A-5 Sequence 5, Appli
12	13	65.0	46	16	US-09-253-006A-5 Sequence 5, Appli
13	13	65.0	46	18	US-09-461-908-5 Sequence 5, Appli
14	13	65.0	46	41	US-10-193-209-5 Sequence 5, Appli
15	12	60.0	21	1	PCT-US02-25940-14041 Sequence 14041, A
16	12	60.0	21	42	US-10-227-563-14041 Sequence 14041, A
C 17	12	60.0	25	26	US-09-660-220-6083 Sequence 6083, Ap
C 18	12	60.0	25	26	US-09-660-220-112404 Sequence 112404,
C 19	12	60.0	25	26	US-09-660-220-112414 Sequence 112414,
C 20	12	60.0	25	36	US-09-956-584-235506 Sequence 235506,
C 21	12	60.0	25	36	US-09-956-584-235507 Sequence 235507,

Sequence 71218, A
Sequence 2716, Ap
Sequence 80128, A
Sequence 248486,
Sequence 248492,
Sequence 164100,
Sequence 205836,
Sequence 230113,
Sequence 244953,
Sequence 438619,
Sequence 615469,
Sequence 625356,
Sequence 654361,
Sequence 13, Appl
Sequence 14042, A
Sequence 14042, A
Sequence 35075, A
Sequence 11591, A
Sequence 11591, A
Sequence 11591, A
Sequence 11591, A
Sequence 13, Appl
Sequence 64, Appl
Sequence 13, Appl
Sequence 14, Appl

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="oligo 16bc"
PCT-US97-23619-7

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTTTCGCGGTGGCAG 20
Db 1 CCAACTTTCGCGGTGGCAG 20

RESULT 2
US-08-770-564A-7
Sequence 7, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-7

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTTTCGCGGTGGCAG 20
Db 1 CCAACTTTCGCGGTGGCAG 20

RESULT 3
PCT-US97-23619-5

Sequence 71218, A
Sequence 2716, Ap
Sequence 80128, A
Sequence 248486,
Sequence 248492,
Sequence 164100,
Sequence 205836,
Sequence 230113,
Sequence 244953,
Sequence 438619,
Sequence 615469,
Sequence 625356,
Sequence 654361,
Sequence 13, Appl
Sequence 14042, A
Sequence 14042, A
Sequence 35075, A
Sequence 11591, A
Sequence 11591, A
Sequence 11591, A
Sequence 11591, A
Sequence 13, Appl
Sequence 64, Appl
Sequence 13, Appl
Sequence 14, Appl

US-60-232-638-71218
US-60-233-620-2716
US-60-233-620-80128
US-60-234-017-248486
US-60-234-017-248492
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US-60-353-987-625356
US-60-353-987-654361
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US-10-227-563-14042
US-09-404-520-35075
US-09-703-708-11591
US-60-164-320-11591
US-60-183-791-11591
US-07-623-729A-13
US-07-748-564A-64
US-08-473-020-13
US-09-861-159-14

ALIGNMENTS

RESULT 1
PCT-US97-23619-7
Sequence 7, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

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; Sequence 5, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "oligo 16"
PCT-US97-23619-5

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGGGTGGCAG 20
Db 11 CCAACTCTTCGGGTGGCAG 30

RESULT 4
US-08-770-564A-5
; Sequence 5, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-5

Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGGGTGGCAG 20
Db 11 CCAACTCTTCGGGTGGCAG 30

RESULT 5
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; Sequence 105231, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-956-604-105231

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Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGGGTGGCA 19
Db 21 CCAACTCTTCGGGTGGCA 4

RESULT 6
US-09-956-604A-105231/c
; Sequence 105231, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
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; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604A-105231

Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
Db      21 CAACTCTTCGCGGTGGCA 4

RESULT 7
US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604B-105231

Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
Db      21 CAACTCTTCGCGGTGGCA 4

RESULT 8
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

Query Match          90.0%; Score 18; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
Db      21 CAACTCTTCGCGGTGGCA 4

RESULT 9
US-08-521-634-15/c
; Sequence 15, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

Query Match          80.0%; Score 16; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCAACTCTTCGCGGTG 16
Db      16 CCAACTCTTCGCGGTG 1

RESULT 10
US-07-941-648-7

Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAACTCTTCGCGGTGGCA 19
Db      21 CAACTCTTCGCGGTGGCA 4
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; Sequence 7, Application US/07941648
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,648
; FILING DATE: 19920908
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: oligonucleotide
; US-07-941-648-7

Query Match 65.0%; Score 13; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGCGGT 15
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Db 25 AACTCTTCGCGGT 37

RESULT 11
US-08-441-893A-5
; Sequence 5, Application US/08441893A
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh 7200/90

; OPERATING SYSTEM: System 7.6
; SOFTWARE: Microsoft Word of Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,893A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; US-08-441-893A-5

Query Match 65.0%; Score 13; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGCGGT 15
|||
Db 25 AACTCTTCGCGGT 37

RESULT 12
US-09-252-006A-5
; Sequence 5, Application US/09252006A
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,006A
FILING DATE: 16-FEBRUARY-1999
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/441,893
FILING DATE: 16-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 05-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,415
FILING DATE: 16-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/091,519
FILING DATE: 12-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,211
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2003-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-09-252-006A-5

Query Match 65.0%; Score 13; DB 16; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37

RESULT 13
US-09-461-908-5
Sequence 5, Application US/09461908
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Cosman, David J.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/199,209
FILING DATE: 19-Jul-2002

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,908
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/091,519
FILING DATE:
APPLICATION NUMBER: US/07/701,415
FILING DATE:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 06-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31680
REFERENCE/DOCKET NUMBER: 2003-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-09-461-908-5

Query Match 65.0%; Score 13; DB 18; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37

RESULT 14
US-10-199-209-5
Sequence 5, Application US/10199209
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Cosman, David J.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/199,209
FILING DATE: 19-Jul-2002


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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
US-10-199-209-5

Query Match      65.0%; Score 13; DB 41; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  AACCTTTCGCGGT 15
Db      25  AACCTTTCGCGGT 37

RESULT 15
PCT-US02-25940-14041
; Sequence 14041, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14041
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1691485)...(1691505)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 16380
PCT-US02-25940-14041

Query Match      60.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7  CTTTCGCGGTGGC 18
Db      9  CTTTCGCGGTGGC 20

Search completed: June 23, 2003, 16:08:20
Job time : 1678.53 secs
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-7
Perfect score: 20
Sequence: 1 CCAACTCTTCGCGTGGCAG 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents NA New.*

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- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
- 11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	80.0	21	1	PCT-US03-04088-588
C 2	16	80.0	23	1	PCT-US03-04088-530
C 3	14	70.0	19	1	PCT-US03-04088-258
C 4	14	70.0	21	1	PCT-US03-04088-593
C 5	14	70.0	25	12	US-60-427-836-401411
C 6	13	65.0	19	1	PCT-US03-04088-22
C 7	13	65.0	19	1	PCT-US03-04088-286
C 8	13	65.0	46	10	US-10-199-209A-5
C 9	12	60.0	21	10	US-10-367-892-14041
C 10	12	60.0	23	1	PCT-US03-04088-522
C 11	12	60.0	25	6	US-09-660-222-6083
C 12	12	60.0	25	6	US-09-660-222-112404
C 13	12	60.0	25	6	US-09-660-222-112414
C 14	12	60.0	25	7	US-09-953-570-71217
C 15	12	60.0	25	7	US-09-954-445A-2716
C 16	12	60.0	25	7	US-09-954-445A-80128
C 17	12	60.0	25	9	US-10-098-263B-31566
C 18	12	60.0	25	9	US-10-355-577-164100
C 19	12	60.0	25	9	US-10-355-577-205836
C 20	12	60.0	25	9	US-10-355-577-230113

C 21	12	60.0	25	9	US-10-355-577-244953	Sequence 244953,
C 22	12	60.0	25	9	US-10-355-577-438619	Sequence 438619, Ap
C 23	12	60.0	25	9	US-10-355-577-615469	Sequence 615469,
C 24	12	60.0	25	9	US-10-355-577-625356	Sequence 625356,
C 25	12	60.0	25	9	US-10-355-577-654361	Sequence 654361,
C 26	12	60.0	25	12	US-60-427-808-942586	Sequence 942586,
C 27	12	60.0	25	12	US-60-427-836-250708	Sequence 250708,
C 28	12	60.0	25	12	US-60-427-836-250709	Sequence 250709,
C 29	12	60.0	25	12	US-60-427-836-582453	Sequence 582453,
C 30	12	60.0	25	12	US-60-427-836-648877	Sequence 648877,
C 31	12	60.0	36	10	US-10-367-892-14042	Sequence 14042, A
C 32	11	55.0	15	10	US-10-299-054A-6945	Sequence 6945, Ap
C 33	11	55.0	15	10	US-10-299-054A-8164	Sequence 8164, Ap
C 34	11	55.0	17	10	US-10-299-054A-8610	Sequence 8610, Ap
C 35	11	55.0	17	10	US-10-299-054A-8620	Sequence 8620, Ap
C 36	11	55.0	22	9	US-10-310-188-70539	Sequence 70539, A
C 37	11	55.0	22	10	US-10-418-401-37	Sequence 37, Appl
C 38	11	55.0	24	9	US-10-310-188-7604	Sequence 7604, Ap
C 39	11	55.0	24	9	US-10-310-188-44232	Sequence 44232, A
C 40	11	55.0	25	7	US-09-953-570-48753	Sequence 48753, A
C 41	11	55.0	25	7	US-09-953-570-48758	Sequence 48758, A
C 42	11	55.0	25	7	US-09-953-570-126899	Sequence 126899,
C 43	11	55.0	25	7	US-09-953-570-126906	Sequence 126906,
C 44	11	55.0	25	7	US-09-953-570-129922	Sequence 129922,
C 45	11	55.0	25	7	US-09-953-570-134925	Sequence 134925,

ALIGNMENTS

RESULT 1

PCT-US03-04088-588/c
; Sequence 588, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 588
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-588

Query Match 80.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGGGTGGCAG 20
|||||
Db 21 CTCTTCGGGTGGCAG 6

RESULT 2
PCT-US03-04088-530/c
; Sequence 530, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 530
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-530

Query Match 80.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.7; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0

QY 5 CTCTTCGGGTGGCAG 20
|||||
Db 23 CTCTTCGGGTGGCAG 8

RESULT 3
PCT-US03-04088-258/c
; Sequence 258, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 258
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-258

Query Match 70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCGGGTGGCAG 20
|||||
Db 19 CTTCGGGTGGCAG 6

RESULT 4
PCT-US03-04088-593
; Sequence 593, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 593
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
PCT-US03-04088-593

Query Match 70.0%; Score 14; DB 1; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTCGGGTGGCAG 20
||::|||:|||||

Db 1 CUUCGCGTGGCAG 14

RESULT 5
US-60-427-836-401411
; Sequence 401411, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 401411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-401411

Query Match 70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGCGTGGCA 19
Db 4 TCTTCGCGTGGCA 17

RESULT 6
PCT-US03-04088-22/c
; Sequence 22, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense
PCT-US03-04088-22

Query Match 65.0%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCCGCGTGGCAG 20
Db 1 UUCGCGGUGGCAG 13

RESULT 8
US-10-199-209A-5
; Sequence 5, Application US/10199209A
; GENERAL INFORMATION:
; APPLICANT: Sime, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Db 19 TTCGCGTGGCAG 7

RESULT 7
PCT-US03-04088-286
; Sequence 286, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
PCT-US03-04088-286

Query Match 65.0%; Score 13; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 5.6e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCGCGTGGCAG 20
Db 1 UUCGCGGUGGCAG 13

RESULT 8
US-10-199-209A-5
; Sequence 5, Application US/10199209A
; GENERAL INFORMATION:
; APPLICANT: Sime, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209A
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209A-5-

Query Match 65.0%; Score 13; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGT 15
Db 25 AACTCTTCGCGGT 37

RESULT 9
US-10-367-892-14041
; SEQUENCE 14041, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14041
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1691485)...(1691505)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 16380
US-10-367-892-14041

Query Match 60.0%; Score 12; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTGCGGTGGC 18
Db 7 CTTGCGGTGGC 18

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Db 9 CTTGCGGTGGC 20

RESULT 10
PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 60.0%; Score 12; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGC 12
Db 12 CCAACTCTTCGC 1

RESULT 11
US-09-660-222-6083/c
; Sequence 6083, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6083
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D25217
US-09-660-222-6083

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Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGCGCGGTGGCA 19
| | | | | | | | | |
Db 17 TTGCGCGGTGGCA 6

RESULT 12

US-09-660-222-112404/c
; Sequence 112404. Application US/09660222

; GENERAL INFORMATION:

; APPLICANT: Mittmann et al.

; TITLE OF INVENTION: Methods of Genetic Analysis of Human

; FILE REFERENCE: 3102.1

; CURRENT APPLICATION NUMBER: US/09/660,222

; PRIOR FILING DATE: 2000-09-12

; PRIOR APPLICATION NUMBER: 60/164,973

; PRIOR FILING DATE: 1999-11-11

; NUMBER OF SEQ ID NOS: 140981

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 112404

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo Sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank X06617

US-09-660-222-112404

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTG 16
| | | | | | | | | |
Db 22 CTCTTCGCGGTG 11

RESULT 13

US-09-660-222-112414/c

; Sequence 112414. Application US/09660222

; GENERAL INFORMATION:

; APPLICANT: Mittmann et al.

; TITLE OF INVENTION: Methods of Genetic Analysis of Human

; FILE REFERENCE: 3102.1

; CURRENT APPLICATION NUMBER: US/09/660,222

; PRIOR FILING DATE: 2000-09-12

; PRIOR APPLICATION NUMBER: 60/164,973

; PRIOR FILING DATE: 1999-11-11

; NUMBER OF SEQ ID NOS: 140981

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 112414

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo Sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank X06617

US-09-660-222-112414

Query Match 60.0%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTG 16
| | | | | | | | | |
Db 16 CTCTTCGCGGTG 5

RESULT 14

US-09-953-570-71217

; Sequence 71217. Application US/09953570

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110.1

; CURRENT APPLICATION NUMBER: US/09/953,570

; PRIOR FILING DATE: 2001-09-13

; PRIOR APPLICATION NUMBER: 60/232,638

; NUMBER OF SEQ ID NOS: 138410

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 71217

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces Cerevisiae

US-09-953-570-71217

Query Match 60.0%; Score 12; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCTTCGCGGTGG 17
| | | | | | | | | |
Db 3 TCTTCGCGGTGG 14

RESULT 15

US-09-954-445A-2716

; Sequence 2716. Application US/09954445A

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana

; FILE REFERENCE: 3116.1

; CURRENT APPLICATION NUMBER: US/09/954,445A

; CURRENT FILING DATE: 2000-09-17

; PRIOR APPLICATION NUMBER: 60/233,620

; PRIOR FILING DATE: 2000-09-18

; NUMBER OF SEQ ID NOS: 131820

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 2716

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-954-445A-2716

Query Match 60.0%; Score 12; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACTCTTCGCGGT 15
| | | | | | | | | |
Db 13 ACTCTTCGCGGT 24

Search completed: June 23, 2003, 19:12:11

Job time : 877.928 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGGCAG 20

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esti:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	55.0	12	13	BM398341
2	11	55.0	19	13	BM401213
3	11	55.0	20	13	BM395007
4	11	55.0	26	13	BM399150
5	11	55.0	33	13	BM398611
6	11	55.0	34	17	AL759526 Arabidops

c

7	11	55.0	37	13	BJ063841
8	11	55.0	40	17	BH851915
c	9	11	44	13	BM400948
10	11	55.0	45	13	BM397151
11	11	55.0	49	9	AA813480
12	11	55.0	50	9	AU106839
13	10	50.0	17	13	BM396493
14	10	50.0	17	13	BM396941
c	15	10	18	14	BM675715
16	10	50.0	20	13	BM400293
17	10	50.0	20	13	BM400757
18	10	50.0	21	13	BM401335
19	10	50.0	23	17	AZ331549
20	10	50.0	23	17	AZ627985
21	10	50.0	24	13	BM399103
22	10	50.0	25	13	BM397307
23	10	50.0	26	13	BM397299
24	10	50.0	29	13	BM400082
25	10	50.0	33	13	BM396856
26	10	50.0	41	13	BM398089
27	10	50.0	42	13	BM400119
28	10	50.0	44	17	AZ309736
29	10	50.0	45	13	BI331734
30	10	50.0	45	17	AQ073648
31	10	50.0	45	17	AZ653181
32	10	50.0	49	14	BQ274449
33	10	50.0	50	9	AA717501
34	10	50.0	50	9	AU102550
35	10	50.0	50	9	AU102613
c	36	10	50	9	AU107631
37	10	50.0	50	9	AU107632
38	10	50.0	50	14	BQ473036
c	39	10	50	14	D43085
40	9	45.0	10	13	BM396011
41	9	45.0	10	13	BM398849
42	9	45.0	11	13	BM396384
43	9	45.0	11	13	BM397892
44	9	45.0	12	13	BM395899
45	9	45.0	12	13	BM395918

ALIGNMENTS

RESULT 1	BM398341	12 bp	mRNA	linear	EST 17-JAN-2002
LOCUS	5009-0-44-D05.t.2	Chilcoat/Turkewitz	CDNA	(large fraction)	
DEFINITION	Tetrahymena thermophila	CDNA, mRNA sequence.			
ACCESSION	BM398341				
VERSION	BM398341.1	GI:18198394			
KEYWORDS	EST.				
SOURCE	Tetrahymena thermophila.				
ORGANISM	Tetrahymena thermophila				
REFERENCE	1 (bases 1 to 12)				
AUTHORS	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobucher, L.				
TITLE	EST from Tetrahymena thermophila, strain CU428.1, growing cells				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkew@midway.uchicago.edu Seq primer: T3.				
FEATURES	1..12	Location/Qualifiers			
source	/organism="Tetrahymena thermophila"				
	/strain="CU428.1"				

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/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      1 a      4 c      6 g      1 t
ORIGIN

Query Match      55.0%; Score 11; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
      |||||
Db      2 CGCGGTGGCAG 12

RESULT 2
BM401213
LOCUS
DEFINITION
5009-0-84-C02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM401213
VERSION
BM401213.1 GI:18201266
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..20
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/strain="CU428.1"
/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      3 a      5 c      8 g      3 t
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Query Match      55.0%; Score 11; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
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Db      9 CGCGGTGGCAG 19

RESULT 3
BM395007
LOCUS
DEFINITION
50072-2-7-A08.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395007
VERSION
BM395007.1 GI:18195060
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..26
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      8 a      5 c      10 g      3 t
ORIGIN

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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..20
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      3 a      7 c      6 g      4 t
ORIGIN

Query Match      55.0%; Score 11; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCGGTGGCAG 20
      |||||
Db      5 CGCGGTGGCAG 15

RESULT 4
BM399150
LOCUS
DEFINITION
5009-0-54-All.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM399150
VERSION
BM399150.1 GI:18199203
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..26
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      8 a      5 c      10 g      3 t
ORIGIN

```

Query Match 55.0%; Score 11; DB 13; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
 |||||
 Db 16 CGCGGTGGCAG 26

RESULT 5
 BM398611
 LOCUS
 DEFINITION 5009-0-47-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 tetrahymena thermophila cDNA, mRNA sequence.
 ACCSSSTON BM398611.1 GI:18198664
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E., Frankel
 J. and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source
 1..33
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /notes="Vector: Bluescript 2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 5 a 10 c 12 g 6 t

Query Match 55.0%; Score 11; DB 13; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
 |||||
 Db 9 CGCGGTGGCAG 19

RESULT 6
 AL759526/c
 LOCUS
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-188A07-014624,
 genomic survey sequence.
 ACCSSSTON AL759526.1 GI:21497874
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Arabidopsis thaliana
 thale cress.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1
 AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
 and Weisshaar, B.
 TITLE A pipeline for automated high-throughput generation of PSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

transformed lines
 Unpublished
 2
 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 34)
 Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
 Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene Atlg07990. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/
 Location/Qualifiers
 1..34
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT 10 a 9 c 9 g 6 t

ORIGIN
 Query Match 55.0%; Score 11; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGCGGTG 16
 |||||
 Db 13 TCTTCGCGGTG 3

RESULT 7
 BJ063841
 LOCUS
 DEFINITION laevis cDNA clone XLO77114 5', mRNA sequence.
 ACCSSSTON BJ063841.1 GI:17471031
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Xenopus laevis
 African clawed frog.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers

```

source
1. 37
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL077114"
/library="NIBB Mochii normalized Xenopus tailbud"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT      5 a 15 c 3 g 13 t 1 others
ORIGIN
Query Match      55.0%; Score 11; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCG 11
    |||||
Db 24 CCAACTCTTCG 34

RESULT 8
LOCUS      BH851915/c
DEFINITION SALK_073707.54.25.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_073707.54.25.x, DNA
            sequence.
ACCESSION  BH851915
VERSION     BH851915.1 GI:21422786
KEYWORDS   GSS.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1 (bases 1 to 40)
AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL    Unpublished (2001)
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: eckers@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At5g46110.
            Class: TDNA tagged.
FEATURES   Location/Qualifiers
            source          1..40
                        /organism="Arabidopsis thaliana"
                        /strain="Columbia 0"
                        /db_xref="taxon:3702"
                        /clone="SALK_073707.54.25.x"
                        /note="PCR was performed on Arabidopsis thaliana lines
                        each of which contains one or more TDNA insertion
                        elements. The resultant fragment for each line was
                        directly sequenced to determine the genomic sequence at
                        the site of insertion. Details of the protocols used can
                        be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      7 a 11 c 12 g 10 t
ORIGIN
Query Match      55.0%; Score 11; DB 17; Length 40;

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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCGCGGTGGC 18
    |||||
Db 27 TTCGCGGTGGC 17

RESULT 9
LOCUS      BM400948
DEFINITION 5009-0-80-E05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM400948
VERSION     BM400948.1 GI:18201001
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila.
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 44)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Unpublished (2002)
COMMENT    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES   Location/Qualifiers
            source          1..44
                        /organism="Tetrahymena thermophila"
                        /strain="CU428.1"
                        /db_xref="taxon:5911"
                        /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                        /note="Vector: Bluescript2 SK+; Details on library
                        preparation can be found in Chilcoat and Turkewitz (2001)
                        Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      10 a 11 c 14 g 8 t 1 others
ORIGIN
Query Match      55.0%; Score 11; DB 13; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCAG 20
    |||||
Db 15 CGCGGTGGCAG 25

RESULT 10
LOCUS      BM397151
DEFINITION 5009-0-29-F01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397151
VERSION     BM397151.1 GI:18197204
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila.
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 45)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Unpublished (2002)
COMMENT    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology

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University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

FEATURES

source

Location/Qualifiers
1. .45
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
10 a 11 c 15 g 9 t

BASE COUNT

10 a 11 c 15 g 9 t

ORIGIN

Query Match 55.0%; Score 11; DB 13; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CGCGGTGGCAG 20
Db 16 CGCGGTGGCAG 26

RESULT 11

AA813480

LOCUS

AA813480 49 bp mRNA linear EST 31-DEC-1998
a167809.s1 Soares testis NHT Homo sapiens cDNA clone 1375864 3',
similar to SW:CAV3_MOUSE P51637 CAVEOLIN-3 ; mRNA sequence.

ACCESSION

AA813480

VERSION

AA813480.1 GI:2882165

KEYWORDS

EST.

SOURCE

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-i@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 1418 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .49

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="1375864"

/clone_lib="Soares_testis_NHT"

/sex="male"

/lab host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, inc., and primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAATGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

FEATURES

source

Location/Qualifiers

1. .49

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="1375864"

/clone_lib="Soares_testis_NHT"

/sex="male"

/lab host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, inc., and primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAATGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT

7 a 21 c 11 g 10 t

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACTCTTCGGG 14

Db 28 ACTCTTCGGG 38

RESULT 12

AU106839

LOCUS

AU106839 50 bp mRNA linear EST 30-AUG-2001
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT08593, mRNA sequence.

ACCESSION

AU106839

VERSION

AU106839.1 GI:13556360

KEYWORDS

EST.

SOURCE

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, T., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata

, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki

, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, T., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

, S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="KAT08593"

/note="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylformate treated U937 cells"

13 a 14 c 17 g 6 t

Query Match 55.0%; Score 11; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTCTTCG 11

Db 29 CCAACTCTTCG 39

RESULT 13

BM396493

LOCUS

BM396493 14 bp mRNA linear EST 17-JAN-2002
5009-0-21-B08.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM396493

VERSION

BM396493.1 GI:18196516

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila.

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 14)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

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University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

Location/Qualifiers

1..14

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

3 a 5 c 5 g 1 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 10; DB 13; Length 14;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 5 CGCGGTGGCA 14

1..18

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="CSEQFL35 adipose"

/tissue_type="adipose tissue"

/note="Organ: adipose tissue; Vector: pBluescript SK+;

Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert

(5'-NNN...NNNinsert)

CGCAATTGAGCTCCACCCGCTGGCGCGGCTCGAG. Sequence 3' of

the inserts (AAGATTCGATATCAAGCTTATCGATACCGTGCCTCGAG.

non-normalized library, sequenced 3' with M13R primer."

2 a 6 c 7 g 3 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 10; DB 14; Length 18;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 10 CGCGGTGGCA 1

1..17

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

2 a 6 c 5 g 4 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 10 CGCGGTGGCA 1

1..17

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

2 a 6 c 5 g 4 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 10 CGCGGTGGCA 1

1..17

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

2 a 6 c 5 g 4 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCGGTGGCA 19

Db 10 CGCGGTGGCA 1

1..17

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

2 a 6 c 5 g 4 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CGCGGTGGCA 1

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preparation can be found in Chilcoat and Turkewitz (2001)

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preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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/note="Vector: Bluescript2 SK+; Details on library

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

2 a 6 c 5 g 4 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

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/organism="Tetrahymena thermophila"

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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BASE COUNT

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/organism="Tetrahymena thermophila"

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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BASE COUNT

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Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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BASE COUNT

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/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/organism="Tetrahymena thermophila"

/strain="CU428.1"

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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	13.4	67.0	46	1	US-08-106-507-7
7	13.4	67.0	46	1	US-08-442-043A-5
8	13.4	67.0	46	5	PCT-US91-03478-5
9	13.2	66.0	36	3	US-08-833-167-69
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30 12 60.0 25 1 US-08-623-891-81 Sequence 81, Appl
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32 12 60.0 25 4 US-09-634-262-81 Sequence 81, Appl
33 11.8 59.0 21 4 US-09-536-936-3 Sequence 3, Appl
34 11.8 59.0 22 4 US-09-240-918-65 Sequence 65, Appl
35 11.8 59.0 25 1 US-08-977-818-16 Sequence 16, Appl
36 11.8 59.0 25 2 US-08-670-274B-16 Sequence 16, Appl
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45 11.8 59.0 46 3 US-08-931-869-39 Sequence 39, Appl

ALIGNMENTS

RESULT 1
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; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-7

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, SOFTWARE: Patent In Release #1.24
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, FILING DATE:
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, PRIOR APPLICATION DATA:
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, FILING DATE:
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, APPLICATION NUMBER: US 07/534,199
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, FILING DATE: 06-JUN-1990
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/573,576
;; FILING DATE: 24-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/627,071
;; FILING DATE: 13-DEC-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wight, Christopher L.
;; REGISTRATION NUMBER: 31680
;; REFERENCE/DOCKET NUMBER: 2003-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-587-5570
;; TELEFAX: 206-233-0644
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 46 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
US-08-091-519-5

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; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
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; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
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; LENGTH: 46 base pairs
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;; ANTI-SENSE: NO
;; IMMEDIATE SOURCE:
;; CLONE: oligonucleotide
US-08-106-507-7

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RESULT 7
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; Sequence 5, Application US/08442043A
; Patent No. 5767064
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; APPLICATION NUMBER: US/08/442,043A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
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; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

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Db 23 CAAACTCTTCGGGT 37
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; Sequence 69, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
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; MOLECULE TYPE: other nucleic acid
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; Sequence 69, Application US/09344837A

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-442-043A-5
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; Sequence 5, Application PC/TUS9103478
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.24
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; FILING DATE: 19910517
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; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; ANTI-SENSE: N
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; Patent No. 6358505
; GENERAL INFORMATION:
; APPLICANT: ZUREL, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. CHRISTOPHER BAUER
; ADDRESSEE: MONSANTO/G. D. SEARLE & CO.,
; ADDRESSEE: PATENT DEPARTMENT CENTRAL
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
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; FILING DATE: 25-JUN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. CHRISTOPHER BAUER
; REFERENCE/DOCKET NUMBER: 2907/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 636-737-6257
; TELEFAX: 636-737-5452
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA (synthetic)"
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Query Match 66.0%; Score 13.2; DB 4; Length 36;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

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QY 1 CCAACTTTCGGGTGTC 18
   ||| ||| ||| ||| |||
Db 19 CCAGCTCTCGGGTGC 36

```

```

RESULT 11
US-08-599-252-36
; Sequence 36, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GNIERKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,252

```

```

; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,252
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9053-0001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-599-252-36

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Query Match 64.0%; Score 12.8; DB 1; Length 22;
Best Local Similarity 87.5%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 4 ACTCTTCGGGTGGCA 19
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Db 1 ACTCTTCGGGTGGCA 16

```

```

RESULT 12
PCT-US96-06352-36
; Sequence 36, Application PC/TUS9606352
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GNIERKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06352
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,252

```

FILING DATE: 09-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 9053-0001.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-06352-36

Query Match 64.0%; Score 12.8; DB 5; Length 22;
 Best Local Similarity 87.5%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACTCTTCGGGTGGCA 19
 Db 1 ACTCTTCGGGTGGCA 16

RESULT 13
 PCT-US96-06583-36
 Sequence 36, Application PC/TUS9606583
 GENERAL INFORMATION:
 APPLICANT: DRYNA, DENNIS T.
 APPLICANT: FEDER, JOHN N.
 APPLICANT: GNIERKE, ANDREAS
 APPLICANT: KIMMEL, BRUCE E.
 APPLICANT: THOMAS, WINSTON J.
 APPLICANT: WOLFF, ROGER K.
 TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
 TITLE OF INVENTION: HEMOCHROMATOSIS
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06583
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/599,252
 FILING DATE: 09-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 9053-0001.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-06583-36

Query Match 64.0%; Score 12.8; DB 5; Length 22;
 Best Local Similarity 87.5%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACTCTTCGGGTGGCA 19
 Db 1 ACTCTTCGGGTGGCA 16

RESULT 14
 US-07-807-529A-64
 Sequence 64, Application US/07807529A
 Patent No. 5547669
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 APPLICANT: Morgenstern, Jay
 APPLICANT: Bond, Julian F.
 APPLICANT: Garman, Richard D.
 APPLICANT: Greenstein, Julia L.
 APPLICANT: Kuo, Mei-chang
 APPLICANT: Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
 STREET: One Kendall Square, Building 600
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02139
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/807,529A
 FILING DATE: 19911213
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Channing, Stacey L.
 REGISTRATION NUMBER: 31,095
 REFERENCE/DOCKET NUMBER: IPC-027/imi-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 494-0060
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-07-807-529A-64

Query Match 64.0%; Score 12.8; DB 1; Length 27;
 Best Local Similarity 87.5%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGTGGC 18
 Db 5 AATCTTCGGGTGGC 20

RESULT 15
 US-08-948-381-3
 Sequence 3, Application US/08948381
 Patent No. 6274341

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; GENERAL INFORMATION:
; APPLICANT: Bailey, James E.
; APPLICANT: Fussenegger, Martin
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: A NOVEL CYTOSTATIC PROCESS
; TITLE OF INVENTION: INCREASES THE PRODUCTIVITY OF CULTURED CELLS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,381
; FILING DATE: 14-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 009187-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-948-381-3

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Query Match      63.0%; Score 12.6; DB 4; Length 28;
Best Local Similarity 78.9%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 CCAACTCTTCGCGTGGA 19
Db      4 CGAATCTTCGCGAGGA 22

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Job time : 31.3586 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGGCGTGCAG 20

Scoring table: IDENTITY NUC

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Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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- 10: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	13.4	67.0	46	9	US-10-199-209-5
2	12.8	64.0	27	7	US-08-464-363-64
3	12.6	63.0	20	9	US-09-954-556-39
4	12.6	63.0	24	10	US-09-820-339A-23
5	12.4	62.0	25	9	US-10-098-2638-31566
6	12.2	61.0	20	10	US-09-909-849-17
7	12.2	61.0	21	9	US-09-943-388-21
8	12.2	61.0	21	9	US-10-002-974-50
9	12.2	61.0	21	12	US-10-014-269-50
10	12.2	61.0	23	9	US-10-084-826-37
11	12.2	61.0	23	10	US-09-844-508-37
12	12.2	61.0	25	9	US-10-098-2638-12812
13	12.2	61.0	36	9	US-09-568-756-4
14	12.0	60.0	23	9	US-09-961-001-6
15	12.0	60.0	25	9	US-10-098-2638-46129
16	12.0	60.0	25	9	US-10-098-2638-100241
17	12.0	60.0	25	9	US-10-098-2638-116734
18	12.0	60.0	33	9	US-09-416-579A-11
19	11.8	59.0	25	9	US-10-098-2638-47805

ALIGNMENTS

RESULT 1

US-10-199-209-5
; Sequence 5, Application US/10199209
; Publication No. US2003006016A1

GENERAL INFORMATION:

APPLICANT: Sims, John E.
Cosman, David J.
Lupton, Stephen D.
Mosley, Bruce A.
Dower, Steven K.

TITLE OF INVENTION: Type II Interleukin-1 Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/199,209

FILING DATE: 19-Jul-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/461,908

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/091,519

FILING DATE: <Unknown>

APPLICATION NUMBER: US/07/701,415

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/534,193

FILING DATE: 06-JUN-1990

APPLICATION NUMBER: US 07/573,576

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: US 07/627,071

FILING DATE: 13-DEC-1990

ATTORNEY/AGENT INFORMATION:

Sequence 54377, A
Sequence 65405, A
Sequence 65406, A
Sequence 84572, A
Sequence 87104, A
Sequence 115897, A
Sequence 125149, A
Sequence 16, Appli
Sequence 9, Appli
Sequence 1234, Ap
Sequence 5, Appli
Sequence 116, App
Sequence 12433, A
Sequence 30410, A
Sequence 31554, A
Sequence 61048, A
Sequence 121314, A
Sequence 124383, A
Sequence 2279, Ap
Sequence 2528, Ap
Sequence 4623, Ap
Sequence 4831, Ap
Sequence 1061, Ap
Sequence 1134, Ap
Sequence 1303, Ap
Sequence 1362, Ap

NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31680
REFERENCE/DOCKET NUMBER: 2003-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5

Query Match 67.0%; Score 13.4; DB 9; Length 46;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGT 15
| | | | | | | | | | | | | | | |
Db 23 CAAACTCTTCGCGGT 37

RESULT 2
US-08-464-363-64
Sequence 64, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBINOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-464-363-64

Query Match 64.0%; Score 12.8; DB 7; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGTGSC 18
| | | | | | | | | | | | | | | |
Db 5 AATCTTTGCGGTGSC 20

RESULT 3
US-09-954-556-39
Sequence 39, Application US/09954556
Publication No. US20030078219A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Preier
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
FILE REFERENCE: R18-0230
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-556-39

Query Match 63.0%; Score 12.6; DB 9; Length 20;
Best Local Similarity 78.9%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
| | | | | | | | | | | | | | | |
Db 2 CCAACTGATCAGCGCGCA 20

RESULT 4
US-09-820-339A-23/c
Sequence 23, Application US/09820339A
Patent No. US20020081652A1
GENERAL INFORMATION:
APPLICANT: FUCHS, Sara
APPLICANT: BARCHAN, Dora
APPLICANT: SOUROUJON, Miriam
TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND THE
TITLE OF INVENTION: FOR TREATMENT OF MYASTHENIA GRAVIS
FILE REFERENCE: FUCHS-2A
CURRENT APPLICATION NUMBER: US/09/820,339A
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 09/423,398
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: PCT/IL98/00211
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-820-339A-23

Query Match 63.0%; Score 12.6; DB 10; Length 24;
Best Local Similarity 78.9%; Pred. No. 3e+03;


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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GAPDH probe
; US-09-844-508-37

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TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 408-2500
 TELEFAX: (212) 765-2519
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-568-756-4

Query Match 61.0%; Score 12.2; DB 9; Length 36;
 Best Local Similarity 82.4%; Pred. No. 4.8e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AACTCTTCGGGTGGCA 19
 Db 26 AACTCTACTCGGTGGCA 10

RESULT 14

US-09-961-001-6
 ; Sequence 6, Application US/09961001
 ; Publication No. US20030109466A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF KSR EXPRESSION
 ; FILE REFERENCE: RTS-0280
 ; CURRENT APPLICATION NUMBER: US/09/961,001
 ; CURRENT FILING DATE: 2001-09-20
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 6
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR Probe
 US-09-961-001-6

Query Match 60.0%; Score 12; DB 9; Length 23;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGGGTGGCAG 20
 Db 3 CCAAGTCTGCTGTCGCAG 22

RESULT 15

US-10-098-263B-46129/c
 ; Sequence 46129, Application US/10098263B
 ; Publication No. US2003010410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 46129
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-46129

Query Match 60.0%; Score 12; DB 9; Length 25;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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 Db 25 CCAAGTCTTCGAGAGGGTAG 6
 Search completed: June 25, 2003, 22:25:05
 Job time : 61.7968 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1697.05 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGCGGTGGCAG 20

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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3	20	100.0	30	PCT-US97-23619-5
4	20	100.0	30	US-08-770-564A-5
5	18	90.0	25	US-09-956-604A-105231
6	18	90.0	25	US-09-956-604A-105231
7	18	90.0	25	US-09-956-604B-105231
8	18	90.0	25	US-09-956-604B-105231
9	16	80.0	24	US-08-521-634-15
10	14.2	71.0	25	US-09-954-427-198291
11	14.2	71.0	25	US-09-956-584-564849
12	14.2	71.0	25	US-09-956-584-564849
13	14.2	71.0	25	US-60-233-166-198291
14	14.2	71.0	25	US-60-234-017-550890
15	14.2	71.0	25	US-60-353-987-207601
16	14.2	71.0	36	US-09-338-248-42
17	14.2	71.0	36	US-09-338-248-42
18	13.8	69.0	25	US-09-660-220-20311
19	13.8	69.0	25	US-09-956-584-564846
20	13.8	69.0	25	US-60-234-017-550884
21	13.8	69.0	25	US-60-353-987-283954

Sequence 7, Appli

Sequence 7, Appli

Sequence 5, Appli

Sequence 105231,

Sequence 105231,

Sequence 105231,

Sequence 86453, A

Sequence 15, Appli

Sequence 198291,

Sequence 564849,

Sequence 198291,

Sequence 550890,

Sequence 207601,

Sequence 42, Appli

Sequence 242, Appli

Sequence 243, Appli

Sequence 20311, A

Sequence 564846,

Sequence 550884,

Sequence 283954,

22	13.8	69.0	27	39	US-10-056-229-224
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25	13.6	68.0	25	36	US-09-956-584-288027
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c	27	13.6	68.0	25	US-09-956-584-487890
c	28	13.6	68.0	25	US-09-956-604-674932
c	29	13.6	68.0	25	US-09-956-604-674932
c	30	13.6	68.0	25	US-09-956-604B-674932
c	31	13.6	68.0	25	US-60-233-166-159814
c	32	13.6	68.0	25	US-60-234-017-294574
c	33	13.6	68.0	25	US-60-234-017-316320
c	34	13.6	68.0	25	US-60-234-017-446035
c	35	13.6	68.0	25	US-60-234-017-490416
c	36	13.6	68.0	25	US-60-234-049-92079
c	37	13.6	68.0	25	US-60-353-987-850409
c	38	13.6	68.0	41	US-09-404-520-28958
c	39	13.6	68.0	41	US-60-353-790-1064
c	40	13.6	68.0	50	US-09-755-374A-17486
c	41	13.6	68.0	50	US-09-755-374A-17488
c	42	13.4	67.0	25	US-09-396-196F-59504
c	43	13.4	67.0	25	US-09-396-196F-59515
c	44	13.4	67.0	25	US-09-396-196G-59504
c	45	13.4	67.0	25	US-09-396-196G-59515

ALIGNMENTS

RESULT 1
PCT-US97-23619-7
Sequence 7, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: * Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..20
; OTHER INFORMATION: /note= "oligo 16bc"
PCT-US97-23619-7

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels

Qy 1 CCAACTCTTCGCGGTGGCAG 20
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Db 1 CCAACTCTTCGCGGTGGCAG 20

RESULT 2
US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-7

```

5.

Sequence 5, Application PC/TUS9723619
 GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: Methods for Detecting and Inhibiting the
 RNA Component of Telomerase

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/23619

FILING DATE: Not yet assigned

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,564

FILING DATE: 20-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,565

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 15389-27PC

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: 1..30

OTHER INFORMATION: /note= "oligo 16"

PCT-US97-23619-5

Query Match 100.0%; Score 20; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGCGTGGCAG 20
 Db 11 CCAACTCTTCGCGTGGCAG 30

RESULT 4

US-08-770-564A-5

Sequence 5, Application US/08770564A

GENERAL INFORMATION:

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ron

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Inhibitory Polynucleotides Directed

Against the RNA Component of Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,564A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002200US

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-564A-5

Query Match 100.0%; Score 20; DB 11; Length 30;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGCGTGGCAG 20
 Db 11 CCAACTCTTCGCGTGGCAG 30

RESULT 5

US-09-956-604-105231/c

Sequence 105231, Application US/09956604

GENERAL INFORMATION:

APPLICANT: Mittmann, Michael

TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

FILE REFERENCE: 3117.1

CURRENT APPLICATION NUMBER: US/09/956,604

CURRENT FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: 60/234,049

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 141629

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 105231

LENGTH: 25

TYPE: DNA

ORGANISM: Escherichia coli

US-09-956-604-105231

Query Match 90.0%; Score 18; DB 36; Length 25;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCAACTCTTCGCGTGGCA 19
 Db 21 CCAACTCTTCGCGTGGCA 4

RESULT 6

US-09-956-604A-105231/c

Sequence 105231, Application US/09956604A

GENERAL INFORMATION:

APPLICANT: Mittmann, Michael

```

; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-956-604A-105231

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Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 CAACTCTTCGCGGTGCA 19
   |||||
Db 21 CAACTCTTCGCGGTGCA 4

```

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RESULT 7
US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-956-604B-105231

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Query Match          90.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CAACTCTTCGCGGTGCA 19
   |||||
Db 21 CAACTCTTCGCGGTGCA 4

```

```

RESULT 8
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
; US-60-234-049-86453

```

```

Query Match          90.0%; Score 18; DB 67; Length 25;

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```

Best Local Similarity 100.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAACTCTTCGCGGTGCA 19
   |||||
Db 21 CAACTCTTCGCGGTGCA 4

```

```

RESULT 9
US-08-521-634-15/c
; Sequence 15, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Funk, Junli
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-521-634-15

```

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Query Match          80.0%; Score 16; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CCAACTCTTCGCGGTG 16
   |||||
Db 16 CCAACTCTTCGCGGTG 1

```

```

RESULT 10
US-09-954-427-198291

```


; Sequence 198291, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-09-954-427-198291

Query Match 71.0%; Score 14.2; DB 36; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGCGGTGGCAG 20
||| ||||| ||||| |||||
DB 7 CAAGACTTCGACGTGGCAG 25

RESULT 11
US-09-956-584-564849/c
; Sequence 564849, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mitmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 564849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-564849

Query Match 71.0%; Score 14.2; DB 36; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
||| ||||| ||||| |||||
DB 20 CCACCTCTTCGCGGTGGTA 2

RESULT 12
US-60-233-166-198291
; Sequence 198291, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA998576
US-60-233-166-198291

Query Match 71.0%; Score 14.2; DB 67; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAACTCTTCGCGGTGGCAG 20
||| ||||| ||||| |||||
DB 7 CAAGACTTCGACGTGGCAG 25

RESULT 13
US-60-234-017-550890/c
; Sequence 550890, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mitmann, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 550890
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV100189
US-60-234-017-550890

Query Match 71.0%; Score 14.2; DB 67; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
||| ||||| ||||| |||||
DB 20 CCACCTCTTCGCGGTGGTA 2

RESULT 14
US-60-353-987-207601/c
; Sequence 207601, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mitmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 207601
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-207601

Query Match 71.0%; Score 14.2; DB 79; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
||| ||||| ||||| |||||
DB 21 CCACCTCTTCAGGGGGCA 3

RESULT 15
US-09-338-248-42/c
; Sequence 42, Application US/09338248
; GENERAL INFORMATION:

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; APPLICANT: Lee, Stephen C
; TITLE OF INVENTION: Method of Producing Permutateins by
; FILE REFERENCE: C 3041
; CURRENT APPLICATION NUMBER: US/09/338,248
; CURRENT FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Synthetic
; US-09-338-248-42

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```

Query Match      71.0%; Score 14.2; DB 17; Length 36;
Best Local Similarity 84.2%; Pred. No. 9e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

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QY      1 CCAACTCTTGGCGGTGGCA 19
         ||| ||| ||| ||| |||
Db      34 CCAGCTCCTCGGGTGGCA 16

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Search completed: June 25, 2003, 06:20:25
Job time : 1698.67 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-7

Perfect score: 20
Sequence: 1 CCAACTCTTCGCGGTGCAG 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	80.0	21	1	PCT-US03-04088-588
C 2	16	80.0	23	1	PCT-US03-04088-530
C 3	14.8	74.0	31	6	US-09-890-648-6
C 4	14.8	74.0	43	10	US-10-299-054A-7701
C 5	14.2	71.0	25	9	US-10-355-577-207601
C 6	14.2	71.0	25	12	US-60-427-808-776553
C 7	14.2	71.0	34	5	US-09-462-405C-4
C 8	14.2	71.0	50	10	US-10-009-792A-5
C 9	14	70.0	19	1	PCT-US03-04088-258
C 10	14	70.0	21	1	PCT-US03-04088-593
C 11	14	70.0	25	12	US-60-427-836-401411
C 12	13.8	69.0	25	6	US-09-660-222-20311
C 13	13.8	69.0	25	9	US-10-355-577-283954
C 14	13.8	69.0	25	12	US-60-427-808-239182
C 15	13.8	69.0	25	12	US-60-427-808-294455
C 16	13.8	69.0	25	12	US-60-427-808-546726
C 17	13.8	69.0	25	12	US-60-427-836-424019
C 18	13.6	68.0	20	6	US-09-964-059B-139
C 19	13.6	68.0	25	9	US-10-355-577-850409
C 20	13.6	68.0	25	12	US-60-427-808-374528

21	13.6	68.0	25	12	US-60-427-808-823538	Sequence 823538,
22	13.6	68.0	25	12	US-60-427-808-823539	Sequence 823539,
23	13.6	68.0	45	12	US-60-288-292-37984	Sequence 37984, A
24	13.4	67.0	25	9	US-10-355-577-386767	Sequence 386767,
25	13.4	67.0	25	9	US-10-355-577-386768	Sequence 386768,
26	13.4	67.0	25	9	US-10-355-577-654361	Sequence 654361,
27	13.4	67.0	46	10	US-10-199-209A-5	Sequence 5, Appli
28	13.2	66.0	25	7	US-09-953-570-1381	Sequence 1381, Ap
C 29	13.2	66.0	25	9	US-10-355-577-225795	Sequence 225795,
C 30	13.2	66.0	25	9	US-10-355-577-270910	Sequence 270910,
C 31	13.2	66.0	25	9	US-10-355-577-599429	Sequence 599429,
C 32	13.2	66.0	25	9	US-10-355-577-600356	Sequence 600356,
C 33	13.2	66.0	25	9	US-10-355-577-806473	Sequence 806473,
C 34	13.2	66.0	25	12	US-60-427-808-12321	Sequence 12321, A
C 35	13.2	66.0	25	12	US-60-427-808-252863	Sequence 252863,
C 36	13.2	66.0	25	12	US-60-427-808-252864	Sequence 252864,
C 37	13.2	66.0	25	12	US-60-427-808-295640	Sequence 295640,
C 38	13.2	66.0	25	12	US-60-427-836-276560	Sequence 276560,
C 39	13.2	66.0	25	12	US-60-427-836-296253	Sequence 296253,
C 40	13.2	66.0	25	12	US-60-427-836-342508	Sequence 342508,
C 41	13.2	66.0	25	12	US-60-427-836-342509	Sequence 342509,
C 42	13.2	66.0	26	9	US-10-089-177-1492	Sequence 1492, Ap
C 43	13.2	66.0	50	9	US-10-325-899-7814	Sequence 7814, Ap
C 44	13	65.0	19	1	PCT-US03-04088-22	Sequence 22, Appli
C 45	13	65.0	19	1	PCT-US03-04088-286	Sequence 286, Appli

ALIGNMENTS

RESULT 1

PCT-US03-04088-588/c
; Sequence 588, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribosome Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 588
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-588

Query Match 80.0%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTCTTCGCGGTGGCAG 20
|||||
Db 21 CTCTTCGCGGTGGCAG 6

RESULT 2

PCT-US03-04088-530/c
; Sequence 530, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 530
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-530

Query Match 80.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 5 CTCTTCGCGGTGGCAG 20
|||||
Db 23 CTCTTCGCGGTGGCAG 8

RESULT 3

US-09-890-648-6
; Sequence 6, Application US/09890648
; GENERAL INFORMATION:
; APPLICANT: Bullerdiek, Jörn
; TITLE OF INVENTION: Preparation for The Prevention and/or Treatment
; TITLE OF INVENTION: of a Tissue Change of Mesenchymal Origin
; FILE REFERENCE: B3960PCT
; CURRENT APPLICATION NUMBER: US/09/890,648
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: description of the artificial sequence: primer ADEIH13AS
US-09-890-648-6

Query Match 74.0%; Score 14.8; DB 6; Length 31;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACTCTTCGCGGTGGCAG 20
|||||
Db 12 AACTCTTCGCGGTGGCAG 29

RESULT 4

US-10-299-054A-7701
; Sequence 7701, Application US/10299054A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/299,054A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11910
; SOFTWARE: Proprietary
; SEQ ID NO 7701
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis complete genome.
; FEATURE:
; LOCATION: (3056464)...(3056506)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 9331
US-10-299-054A-7701

Query Match 74.0%; Score 14.8; DB 10; Length 43;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGC 18
|||||
Db 24 CCAACTCTTCGCGGTAGC 41

RESULT 5

US-10-355-577-207601/c
; Sequence 207601, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 207601
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-207601

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTCTTCGCGGTGGCA 19
|||||
Db 21 CCAACTCTTCAAGGGGGCA 3

RESULT 6

US-60-427-808-776553
; Sequence 776553, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20

```
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 776553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-776553

Query Match          71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAACTTCGCGGTGGCA 20
Db 6 CCAACTTTTCGACAGGCA 24

RESULT 7
US-09-462-405C-4
; Sequence 4, Application US/09462405C
; GENERAL INFORMATION:
; APPLICANT: Hillgenberg, Moritz
; APPLICANT: Loser, Peter
; APPLICANT: Schnieders, Frank
; APPLICANT: Sandig, Volker
; APPLICANT: Strauss, Michael
; TITLE OF INVENTION: Cloning Vectors for Producing Adenoviral Minimal Viruses
; FILE REFERENCE: 101195-13
; CURRENT APPLICATION NUMBER: US/09/462,405C
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: PCT/DE98/01940
; PRIOR FILING DATE: 1998-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-462-405C-4

Query Match          71.0%; Score 14.2; DB 5; Length 34;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTTCGCGGTGGCA 19
Db 10 CCAACTTACTCGTGGCA 28

RESULT 8
US-10-009-792A-5/c
; Sequence 5, Application US/10009792A
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; APPLICANT: JEONG, Ki-Jun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; FILE REFERENCE: HYLEP60.001APC
; CURRENT APPLICATION NUMBER: US/10/009,792A
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-009-792A-5
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Query Match          71.0%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAACTTCGCGGTGGCA 19
Db 23 CCAGCTCCTCGGGTGGCA 5

RESULT 9
PCT-US03-04088-258/c
; Sequence 258, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 258
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-258

Query Match          70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTGCGGTGGCAG 20
Db 19 CTTGCGGTGGCAG 6

RESULT 10
PCT-US03-04088-593
; Sequence 593, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 593
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
PCT-US03-04088-593

Query Match          70.0%; Score 14; DB 1; Length 21;
Best Local Similarity 78.6%; Pred. No. 3.4e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTTGCGGTGGCGAG 20
   |||||
Db 1 CUUCGGGUGGCGAG 14

RESULT 11
US-60-427-836-401411
; Sequence 401411, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 401411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-401411

Query Match          70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCTTCGGGTGGCA 19
   |||||
Db 4 TCTTCGGGTGGCA 17

RESULT 12
US-09-660-222-20311/c
; Sequence 20311, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 20311
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: TIGR HG2663-HT2759
US-09-660-222-20311

Query Match          69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGGGTGG 17
   |||||
Db 18 CCACCTCTTAGGGTGG 2

RESULT 13
US-10-355-577-283954
; Sequence 283954, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UL13
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 283954
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-283954

Query Match          69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAACTCTTCGGGTGG 17
   |||||
Db 3 CCACCTCTTCGAGGAGG 19

RESULT 14
US-60-427-808-239182/c
; Sequence 239182, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 239182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-239182

Query Match          69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACTCTTCGGGTGGCAG 20
   |||||
Db 21 AGTCCTTCGGGTGGCAG 5

RESULT 15
US-60-427-808-294455/c
; Sequence 294455, Application US/60427808
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 294455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-294455

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Query Match      69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      3 AACCTCTTCGGGTGGCA 19
      |||||
Db      21 AACCTCTTCGAGGTAGCA 5

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Search completed: June 26, 2003, 04:15:16
Job time : 479.077 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-6
Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTCTTC 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
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- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR063830 Sequence
2	20	100.0	30	6	AR063829 Sequence
3	12	60.0	20	12	AB069038 Synthetic
4	12	60.0	28	9	S72525 TCR V gamma
5	12	60.0	30	9	HSTCRGV33
6	12	60.0	43	6	AX158160 Sequence
7	12	60.0	46	6	AX158162 Sequence
8	12	60.0	50	6	AX024597 Sequence
9	11	55.0	12	6	A14857 Nucleotide
10	11	55.0	15	6	AR056247 Sequence
11	11	55.0	15	6	AR114005 Sequence
12	11	55.0	18	6	A32455 Synthetic p
13	11	55.0	18	6	A32726 Synthetic d
14	11	55.0	18	6	I19611 Sequence 12
15	11	55.0	18	6	I84271 Sequence 42
16	11	55.0	20	6	A09892 Oligonucleo
17	11	55.0	20	6	A09923 Probe. 1/19
18	11	55.0	20	6	A14859 Nucleotide
19	11	55.0	20	6	AR002212 Sequence
20	11	55.0	20	6	E05218 Probe for g
21	11	55.0	20	6	E16501 PCR primer
22	11	55.0	21	6	AR129457 Sequence
23	11	55.0	21	6	AX110621 Sequence
24	11	55.0	22	6	AX110619 Sequence
25	11	55.0	24	6	A09925 Probe. 1/19
26	11	55.0	24	6	AR171201 Sequence
27	11	55.0	24	6	AX068559 Sequence
28	11	55.0	24	6	AX445836 Sequence
29	11	55.0	25	9	HSA270340
30	11	55.0	27	9	HSTCRGV24
31	11	55.0	30	9	HSTCRGV22
32	11	55.0	30	9	S72587 TCR gamma =
33	11	55.0	30	9	S72591 TCR gamma =
34	11	55.0	36	6	AR148975 Sequence
35	11	55.0	36	6	AR196827 Sequence
36	11	55.0	36	6	AX016752 Sequence
37	11	55.0	36	6	AX016769 Sequence
38	11	55.0	38	6	AR148976 Sequence
39	11	55.0	38	6	AR196828 Sequence
40	11	55.0	38	6	AX016753 Sequence
41	11	55.0	38	6	AX016770 Sequence
42	11	55.0	39	9	HSTCRGV35
43	11	55.0	42	6	AR163562 Sequence
44	11	55.0	49	6	E08684 Oligonucleo
45	11	55.0	49	6	E08686 Oligonucleo

ALIGNMENTS

RESULT 1	AR063830	Sequence 6 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063830	Sequence 6 from patent US 5846723.				
DEFINITION	AR063830	Sequence 6 from patent US 5846723.				
ACCESSION	AR063830	Sequence 6 from patent US 5846723.				
VERSION	AR063830.1	GI:5993138				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Kim,N.Woo., Wu,P., Kealey,J.T., Pruzan,R. and Weinrich,S.L.					
TITLE	Methods for detecting the RNA component of telomerase					
JOURNAL	Patent: US 5846723-A 6 08-DEC-1998;					
FEATURES	Location/Qualifiers					

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source
1. .20
/organism="unknown"
BASE COUNT      5 a      8 c      3 g      4 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
    |||||
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
AR063829
LOCUS      AR063829
DEFINITION Sequence 5 from patent US 5846723.
ACCESSION  AR063829
VERSION     AR063829.1 GI:5993137
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kim,N.WOO., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE       Methods for detecting the RNA component of telomerase
JOURNAL     Patent: US 5846723-A 5 08-DEC-1998;
FEATURES    Location/Qualifiers
            source
            1. .30
            /organism="unknown"
BASE COUNT      6 a      10 c      9 g      5 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
    |||||
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
AB069038
LOCUS      AB069038
DEFINITION Synthetic construct DNA, forward primer for human STS sts-A008J44
            at lp36.
ACCESSION  AB069038.1 GI:15129842
VERSION     AB069038
KEYWORDS   synthetic construct DNA.
SOURCE      artificial sequences.
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
TITLE       A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
JOURNAL     Genomics 74 (1), 55-70 (2001)
MEDLINE     21269192
REFERENCE   2 (bases 1 to 20)
AUTHORS     Horii,A.
TITLE       Direct Submission
JOURNAL     Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES    Location/Qualifiers
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            1. .20
            /organism="synthetic construct"

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misc_feature
1. .20
/db xref="taxon:32630"
/note="forward primer for human STS sts-A008J44 at lp36
sts-A008J44 obtained from clones B316C6, B132G19, B375M9,
Human BAC library RPCI-11"
BASE COUNT      4 a      8 c      1 g      7 t
ORIGIN
Query Match      60.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20
    |||||
Db 2 GCCCAACTCTTC 13

RESULT 4
S72525
LOCUS      S72525/c
DEFINITION TCR V gamma 9-T cell receptor gamma chain (V-J junction) [human,
            mRNA Partial Mutant, 28 nt].
ACCESSION  S72525
VERSION     S72525.1 GI:240432
KEYWORDS   Homo sapiens.
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Holroyd,K.J., Tamura,N., Banks,T., Kirby,M., Okayama,H. and
            Crystal,R.G.
TITLE       Limited diversity of gamma delta T-cell antigen receptor junctional
            region sequences in individuals with sarcoidosis compared to broad
            diversity in normal subjects
JOURNAL     Trans. Assoc. Am. Physicians 103, 102-111 (1990)
MEDLINE     92087348
PUBMED      2151899
REMARK      GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbaq 72525] from the original journal article.
            This sequence comes from Figure 4.
FEATURES    Location/Qualifiers
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            1. .28
            /organism="Homo sapiens"
            /db xref="taxon:9606"
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            /note="T cell receptor gamma chain"
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            /gene="TCR V<gamma>9"
            /note="This sequence comes from Figure 4; conceptual
            translation differs from the translation presented in the
            manuscript"
            /codon_start=2
            /product="T cell receptor gamma chain"
            /protein_id="AAB20598.2"
            /db_xref="GI:7717239"
            /translation="ELWEREELG"
BASE COUNT      5 a      4 c      13 g      6 t
ORIGIN
Query Match      60.0%; Score 12; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20
    |||||
Db 28 GCCCAACTCTTC 17

RESULT 5
HSTCRGV33/c
LOCUS      HSTCRGV33

```

```

DEFINITION H.sapiens mRNA for rearranged TCR-gamma chain V region (VJ).
ACCESSION X69253
VERSION X69253.1 GI:510639
KEYWORDS J-region; N-region; T-cell receptor; T-cell receptor gamma chain;
V-region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 30)
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1992) J. Hvas, La Trobe University,
Neuroimmunology Lab., Dept. of Psych., La Trobe University,
Bundoora, Victoria 3083, AUSTRALIA
REFERENCE 2 (bases 1 to 30)
AUTHORS Hvas, J., Oksenberg, J.R., Fernando, R., Steinman, L. and Bernard, C.C.
TITLE Gamma delta T cell receptor repertoire in brain lesions of patients
with multiple sclerosis
JOURNAL J. Neuroimmunol. 46 (1-2), 225-234 (1993)
MEDLINE 93367035
PUBMED 8395544
FEATURES
    Location/Qualifiers
        1..30
            /organism="Homo sapiens"
            /isolate="MS patient SEL"
            /db_xref="taxon:9606"
            /clone="MSSSELBRASG"
            /tissue_type="brain"
        misc_feature
            1..11
                /note="V-gamma-2 segment"
        misc_feature
            12..16
                /note="N region"
        misc_feature
            17..30
                /note="J-gamma-1.2 segment"
BASE COUNT 8 a 4 c 12 g 6 t
ORIGIN
Query Match: 60.0%; Score 12; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20
    |||||
Db 27 GCCCAACTCTTC 16

RESULT 6
AX158160/c
LOCUS AX158160 43 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1488 from Patent WO0140521.
ACCESSION AX158160
VERSION AX158160.1 GI:14539491
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
TITLE Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0140521-A 1488 07-JUN-2001;
Curagen Corporation (US)
FEATURES
    Location/Qualifiers
        1..43
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
        misc_feature
            18..19
                /note="Nucleotide deleted between bases 18 and 19"
        misc_feature
            19
                /note="Nucleotide deleted between bases 18 and 19"
            Accession number c929694531
            /note="2 of 2 allelic variants (1487 is other entry)"

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BASE COUNT 10 a 14 c 6 g 13 t
ORIGIN
Query Match: 60.0%; Score 12; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
    |||||
Db 28 GACAGAGCCCAA 17

RESULT 7
AX158162/c
LOCUS AX158162 46 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1490 from Patent WO0140521.
ACCESSION AX158162
VERSION AX158162.1 GI:14539493
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
TITLE Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0140521-A 1490 07-JUN-2001;
Curagen Corporation (US)
FEATURES
    Location/Qualifiers
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                /note="Nucleotide deleted between bases 21 and 22"
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            22
                /note="2 of 2 allelic variants (1489 is other entry)"
BASE COUNT 10 a 15 c 6 g 15 t
ORIGIN
Query Match: 60.0%; Score 12; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
    |||||
Db 28 GACAGAGCCCAA 17

RESULT 8
AX024597
LOCUS AX024597 50 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 13 from Patent WO0028021.
ACCESSION AX024597
VERSION AX024597.1 GI:10184737
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 50)
AUTHORS Turecek, P., Schieflinger, F., Schwarz, H.P., Lenting, P.J., van
Mourik, J.A., Pannekoek, H. and Mertens, K.
TITLE A factor viii-polypeptide with factor viii:c-activity
JOURNAL Patent: WO 0028021-A 13 18-MAY-2000;
BAXTER AKTIENGESSELLSCHAFT (AT); TURECEK PETER (AT); SCHIEFLINGER
FRIEDRICH (AT); SCHWARZ HANS PETER (AT); LENTING PETRUS JOHANNES
(NL); MOURIK JAN AART VAN (NL); PANNEKOEK HANS (NL); MERTENS
KOENRAAD (NL)
FEATURES
    Location/Qualifiers
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            /db_xref="taxon:32630"

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BASE COUNT      11 a      16 c      15 g      8 t
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/note="Oligonucleotide"

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Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GAGCCCACTCT 18
      |||
Db      31 GAGCCCACTCT 42

RESULT 9
A14857/c
LOCUS      A14857      12 bp      DNA      linear      PAT 16-MAY-1994
DEFINITION Nucleotide sequence 1 from patent number EP0334694.
ACCESSION  A14857
VERSION     A14857.1 GI:512100
KEYWORDS
SOURCE      unidentified.
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 12)
AUTHORS    Cravador,A., De Vos-Pierreux,M.J. and Bollen,A.
TITLE      Nucleic acid probes with non-radioactive labels, and preparation
           processes
JOURNAL    Patent: EP 0334694-A 1 27-SEP-1989;
           IRE-CELLTARG S.A.; LA REGION WALLONNE
FEATURES   source
           1. .12
           Location/Qualifiers
           /organism="unidentified"
           /db_xref="taxon:32644"
BASE COUNT      0 a      4 c      4 g      4 t
ORIGIN

Query Match      55.0%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACAGAGCCCA 13
      |||
Db      11 GACAGAGCCCA 1

RESULT 10
AR056247
LOCUS      AR056247      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 451 from patent US 5837542.
ACCESSION  AR056247
VERSION     AR056247.1 GI:5981824
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE      Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL    Patent: US 5837542-A 451 17-NOV-1998;
           Location/Qualifiers
           1. .15
           /organism="unknown"
BASE COUNT      3 a      6 c      1 g      5 t
ORIGIN

Query Match      55.0%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCCAACTCTTC 20
      |||
Db      1 CCCAACTCTTC 11

us-08-770-564a-6.oligo.rge

RESULT 11
AR114005
LOCUS      AR114005      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 451 from patent US 6132967.
ACCESSION  AR114005
VERSION     AR114005.1 GI:14094327
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 451 17-OCT-2000;
           Location/Qualifiers
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BASE COUNT      3 a      6 c      1 g      5 t
ORIGIN

Query Match      55.0%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCCAACTCTTC 20
      |||
Db      1 CCCAACTCTTC 11

RESULT 12
A32455
LOCUS      A32455      18 bp      DNA      linear      PAT 07-MAY-1996
DEFINITION Synthetic papillomavirus type 16 E7 probe.
ACCESSION  A32455
VERSION     A32455.1 GI:1567446
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Cros,P., Allibert,P.A., Mandrand,B.F. and Dalbon,P.T.
TITLE      Method for immobilizing a nucleic acid fragment by passive
           adsorption on a solid support, solid support obtained therefrom and
           its utilisation
JOURNAL    Patent: EP 0524864-A 10 27-JAN-1993;
           BIO MERIEUX, Societe anonyme
           Location/Qualifiers
           1. .18
           /organism="synthetic construct"
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BASE COUNT      5 a      7 c      4 g      2 t
ORIGIN

Query Match      55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACAGAGCCCA 13
      |||
Db      4 GACAGAGCCCA 14

RESULT 13
A32726
LOCUS      A32726      18 bp      DNA      linear      PAT 05-JUL-1996
DEFINITION Synthetic detection probe for HPV16 E7 gene.
ACCESSION  A32726
VERSION     A32726.1 GI:1567574
KEYWORDS

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SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630" 2 t
BASE COUNT 5 a 7 c 4 g 2 t
ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. NO. 4.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 4 GACAGAGCCCA 14

Search completed: June 23, 2003, 06:34:16
Job time : 234.051 secs

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
I19611
LOCUS 18 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 12 from patent US 5510084.
ACCESSION I19611
VERSION I19611.1 GI:1599966
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Cross, P., Allibert, P.A., Mandrand, B.P. and Dalbon, P.T.
TITLE Process for immobilizing a nucleic acid fragment by passive attachment to a solid substrate, the solid substrate thus obtained, and its use
JOURNAL Patent: US 5510084-A 12 23-APR-1996;
FEATURES
source
1. .18
Location/Qualifiers
/organism="unknown" 2 t
BASE COUNT 5 a 7 c 4 g 2 t
ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. NO. 4.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 4 GACAGAGCCCA 14

RESULT 15
I84271
LOCUS 18 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 42 from patent US 5695926.
ACCESSION I84271
VERSION I84271.1 GI:3021791
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Cross, P., Allibert, P., Mallet, F., Mabilat, C. and Mandrand, B.
TITLE Sandwich hybridization assays using very short capture probes noncovalently bound to a hydrophobic support
JOURNAL Patent: US 5695926-A 42 09-DEC-1997;
FEATURES
source
1. .18
Location/Qualifiers
/organism="unknown" 2 t
BASE COUNT 5 a 7 c 4 g 2 t
ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. NO. 4.6e+04;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCACTCTTC 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents NA, New.*

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- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
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- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	23	1	PCT-US03-04088-522
C 2	19	95.0	21	1	PCT-US03-04088-540
C 3	19	95.0	21	1	PCT-US03-04088-544
C 4	19	95.0	21	1	PCT-US03-04088-548
C 5	19	95.0	21	1	PCT-US03-04088-552
C 6	19	95.0	21	1	PCT-US03-04088-556
C 7	19	95.0	21	1	PCT-US03-04088-560
C 8	18	90.0	19	1	PCT-US03-04088-23
C 9	18	90.0	19	1	PCT-US03-04088-287
C 10	14	70.0	25	12	US-60-427-808-47221
C 11	14	70.0	25	12	US-60-427-808-699316
C 12	14	70.0	25	12	US-60-427-808-529892
C 13	13	65.0	20	1	PCT-US02-21361-189
C 14	13	65.0	20	9	US-10-188-186-189
C 15	13	65.0	20	9	US-10-160-619-306
C 16	13	65.0	20	9	US-10-160-619-315
C 17	13	65.0	25	6	US-09-660-222-68821
C 18	13	65.0	25	6	US-09-660-222-68822
C 19	13	65.0	25	6	US-09-660-222-68827
C 20	13	65.0	25	6	US-09-660-222-68828

C 21	13	65.0	25	6	US-09-660-222-68829	Sequence 68829, A
C 22	13	65.0	25	9	US-10-355-577-281714	Sequence 281714, A
C 23	13	65.0	25	9	US-10-355-577-534052	Sequence 534052, A
C 24	13	65.0	25	12	US-60-427-808-2606	Sequence 2606, Ap
C 25	13	65.0	25	12	US-60-427-808-435724	Sequence 435724, A
C 26	13	65.0	25	12	US-60-427-808-467623	Sequence 467623, A
C 27	13	65.0	25	12	US-60-427-808-503841	Sequence 503841, A
C 28	13	65.0	25	12	US-60-427-836-9568	Sequence 9568, Ap
C 29	13	65.0	25	12	US-60-427-836-9550	Sequence 9550, A
C 30	13	65.0	25	12	US-60-427-836-198381	Sequence 198381, A
C 31	13	65.0	25	12	US-60-427-836-331174	Sequence 331174, A
C 32	12	60.0	24	9	US-10-293-338-4756	Sequence 4756, Ap
C 33	12	60.0	25	6	US-09-660-222-209	Sequence 209, App
C 34	12	60.0	25	6	US-09-660-222-27816	Sequence 27816, A
C 35	12	60.0	25	6	US-09-660-222-27829	Sequence 27829, A
C 36	12	60.0	25	6	US-09-660-222-28011	Sequence 28011, A
C 37	12	60.0	25	6	US-09-660-222-28022	Sequence 28022, A
C 38	12	60.0	25	7	US-09-953-570-9476	Sequence 9476, Ap
C 39	12	60.0	25	7	US-09-953-570-9478	Sequence 9478, Ap
C 40	12	60.0	25	7	US-09-954-445A-21329	Sequence 21329, A
C 41	12	60.0	25	9	US-10-355-577-72838	Sequence 72838, A
C 42	12	60.0	25	9	US-10-355-577-282353	Sequence 282353, A
C 43	12	60.0	25	9	US-10-355-577-515821	Sequence 515821, A
C 44	12	60.0	25	9	US-10-355-577-558628	Sequence 558628, A
C 45	12	60.0	25	12	US-60-427-808-48673	Sequence 48673, A

ALIGNMENTS

RESULT 1

PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 100.0%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 22 CTGACAGAGCCCAACTCTTC 3

RESULT 2
PCT-US03-04088-540/c
; Sequence 540, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 544
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)-(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-544

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 4
PCT-US03-04088-548/c
; Sequence 548, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 548
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (1)-(1)

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 22 CTGACAGAGCCCAACTCTTC 3

RESULT 2
PCT-US03-04088-540/c
; Sequence 540, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 540
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)-(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-540

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
Db 19 TGACAGAGCCCAACTCTTC 1

RESULT 3
PCT-US03-04088-544
; Sequence 544, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124


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; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
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Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
   |||||
Db 19 TGACAGAGCCCAACTCTTC 1
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RESULT 5
PCT-US03-04088-552
; Sequence 552. Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 552
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
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```
Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
   |||||
Db 1 UGACAGAGCCCAACUCUC 19
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```
RESULT 6
PCT-US03-04088-556/c
; Sequence 556. Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 556
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 2'-deoxy
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; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-556

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Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 TGACAGAGCCCAACTCTTC 20
Db 19 TGACAGAGCCCAACTCTTC 1

```

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RESULT 7
PCT-US03-04088-560
; Sequence 560, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129

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; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 560
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(8)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-560

Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.27;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 8
PCT-US03-04088-23/c
; Sequence 23, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129

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; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 23
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-23

Query Match 90.0%; Score 18; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCT 18
 Db 18 CTGACAGAGCCCAACTCT 1

RESULT 9
 PCT-US03-04088-287
 ; Sequence 287, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT-US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 287
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
 ; OTHER INFORMATION: region
 PCT-US03-04088-287

Query Match 90.0%; Score 18; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.1;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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 Db 2 CUGACAGAGCCCAACUCU 19

RESULT 10
 US-60-427-808-47221
 ; Sequence 47221, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 47221
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-47221

Query Match 70.0%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTT 19
 Db 2 AGAGCCCAACTCTT 15

RESULT 11
 US-60-427-808-699316
 ; Sequence 699316, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 699316
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-699316

Query Match 70.0%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCTTC 20
 Db 3 GAGCCCAACTCTTC 16

RESULT 12
 US-60-427-836-529892/c
 ; Sequence 529892, Application US/60427836
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527
 ; CURRENT APPLICATION NUMBER: US/60/427,836
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 529892
 ; LENGTH: 25
 ; TYPE: DNA


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; APPLICANT: Rothenberg, Mark
; APPLICANT: Shency, Suresh
; APPLICANT: Shimkets, Richard
; APPLICANT: Smithson, Glennnda
; APPLICANT: Spaderna, Steven
; APPLICANT: Spytek, Kimberly
; APPLICANT: Stone, David
; APPLICANT: Vernet, Corine
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-377C
; CURRENT APPLICATION NUMBER: US/10/160,619
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,528
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 539
; SEQ ID NO 306
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer
US-10-160-619-306

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Query Match      65.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      6 AGAGCCCAACTCT 18
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Db      6 AGAGCCCAACTCT 18

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Search completed: June 23, 2003, 19:12:11
Job time : 877.928 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCAACTTTC 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues.

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 71: /cgn2_6/ptodata/2/pna/US6027 COMB.seq.*
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- 74: /cgn2_6/ptodata/2/pna/US6030 COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	30	1	PCT-US97-23619-5
4	20	100.0	30	11	US-08-770-564A-5
5	18	90.0	24	9	US-08-521-634-15
6	13	65.0	25	17	US-09-396-1968-124326
7	13	65.0	25	17	US-09-396-1968-124326
8	13	65.0	25	26	US-09-660-220-66821
9	13	65.0	25	26	US-09-660-220-66822
10	13	65.0	25	26	US-09-660-220-66827
11	13	65.0	25	26	US-09-660-220-66828
12	13	65.0	25	26	US-09-660-220-66829
13	13	65.0	25	36	US-09-956-584-314490
14	13	65.0	25	36	US-09-956-584-314500
15	13	65.0	25	67	US-60-234-017-309805
16	13	65.0	25	67	US-60-234-017-309812
17	13	65.0	25	79	US-60-353-987-281714
18	13	65.0	25	79	US-60-353-987-534052
19	13	65.0	42	29	US-09-724-750-18382
20	13	65.0	42	61	US-60-171-431-18382
21	12	60.0	20	39	US-10-093-311-38

Sequence 6, Appli
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Sequence 66827, A
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Sequence 534052, A
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Sequence 18382, A
Sequence 36, Appli

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;
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..20
; OTHER INFORMATION: /note="oligo 16ab"
PCT-US97-23619-6

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20

RESULT 2
US-08-770-564A-6
; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-6

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20

RESULT 3
PCT-US97-23619-5
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Sequence 5, Application PC/TUS9723619
GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/23619

FILING DATE: Not yet assigned

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,564

FILING DATE: 20-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,565

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 15389-27PC

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: 1..30

OTHER INFORMATION: /note= "oligo 16"

PCT-US97-23619-5

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 4

US-08-770-564A-5

Sequence 5, Application US/08770564A

GENERAL INFORMATION:

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ron

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Inhibitory Polynucleotides Directed

TITLE OF INVENTION: Against the RNA Component of Telomerase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,564A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-0022000US

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-564A-5

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 5

US-08-521-634-15/c

Sequence 15, Application US/08521634

GENERAL INFORMATION:

APPLICANT: Villegonteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/521,634

FILING DATE: 31-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,115

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIORITY APPLICATION DATA: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

Query Match 90.0%; Score 18; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCACTCTTC 20
|||||
DB 24 GACAGAGCCCACTCTTC 7

RESULT 6
US-09-396-196F-124326
Sequence 124326, Application US/09396196F
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196F
CURRENT FILING DATE: 2001-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124326
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196F-124326

Query Match 65.0%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAA 14
|||||
DB 2 TGACAGAGCCCAA 14

RESULT 7
US-09-396-196G-124326
Sequence 124326, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 124326
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-124326

Query Match 65.0%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAA 14
|||||
DB 2 TGACAGAGCCCAA 14

RESULT 8
US-09-660-220-66821/c
Sequence 66821, Application US/09660220
GENERAL INFORMATION:
APPLICANT: Mittmann et al.
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Human
FILE REFERENCE: 3102.1
CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/164,973
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66821
LENGTH: 25
TYPE: DNA
ORGANISM: Homo Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66821

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTC 17
|||||
DB 16 CAGAGCCCACTC 4

RESULT 9
US-09-660-220-66822/c
Sequence 66822, Application US/09660220
GENERAL INFORMATION:
APPLICANT: Mittmann et al.
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Human
FILE REFERENCE: 3102.1
CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/164,973
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66822
LENGTH: 25
TYPE: DNA
ORGANISM: Homo Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66822

Query Match 65.0%; Score 13; DB 26; Length 25;

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Best Local Similarity 100.0%; Pred. No. 3.7e+03; Mismatches 0; Gaps 0; Indels 0;
Matches 13; Conservative 0;

QY 5 CAGAGCCCAACTC 17
DB 13 CAGAGCCCAACTC 1

RESULT 10
US-09-660-220-66827/c
; Sequence 66827, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66827
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66827

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTC 17
DB 19 CAGAGCCCAACTC 7

RESULT 11
US-09-660-220-66828/c
; Sequence 66828, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66828

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTC 17
DB 25 CAGAGCCCAACTC 13

RESULT 12
US-09-660-220-66829/c
; Sequence 66829, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66829
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66829

Query Match 65.0%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTC 17
DB 25 CAGAGCCCAACTC 13

RESULT 13
US-09-584-314490
; Sequence 314490, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 314490
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-314490

Query Match 65.0%; Score 13; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCA 13
DB 1 CTGACAGAGCCCA 13

RESULT 14
US-09-956-584-314500
; Sequence 314500, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 314500
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-314500
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US-09-956-584-314500

Query Match 65.0%; Score 13; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCA 13
|||||
Db 6 CTGACAGAGCCCA 18

RESULT 15

US-60-234-017-309805
; Sequence 309805, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309805
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AW049747
US-60-234-017-309805

Query Match 65.0%; Score 13; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCA 13
|||||
Db 1 CTGACAGAGCCCA 13

Search completed: June 23, 2003, 16:08:19
Job time : 1678.53 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTTTC 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PT_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12	60.0	31	9	US-09-288-971-6
2	12	60.0	31	9	US-09-288-971-10
3	11	55.0	18	10	US-09-969-373-3187
c 4	11	55.0	21	9	US-10-222-334-65
5	11	55.0	24	9	US-09-940-185-2291
c 6	11	55.0	24	10	US-09-898-779-110
7	11	55.0	25	9	US-09-992-665-205
8	11	55.0	25	9	US-10-098-263B-110352
9	11	55.0	26	10	US-09-118-276-16
c 10	11	55.0	36	9	US-09-986-118A-24
c 11	11	55.0	36	9	US-09-824-017-25
c 12	11	55.0	38	9	US-09-986-118A-25
c 13	11	55.0	17	9	US-09-818-875-1383
c 14	10	50.0	17	9	US-09-818-875-1384
c 15	10	50.0	17	9	US-09-818-875-1387
c 16	10	50.0	17	9	US-09-818-875-1388
c 17	10	50.0	17	9	US-09-818-875-1388
c 18	10	50.0	19	9	US-10-093-958-22
c 19	10	50.0	19	9	US-10-291-022-2

c 20	10	50.0	20	9	US-10-090-011-45	Sequence 45, Appl
21	10	50.0	20	9	US-09-915-814-161	Sequence 161, App
22	10	50.0	20	10	US-09-263-959-1126	Sequence 1126, Ap
23	10	50.0	21	9	US-09-853-526-420	Sequence 420, App
24	10	50.0	21	9	US-10-082-804-3	Sequence 3, Appli
25	10	50.0	21	9	US-09-909-567B-23	Sequence 23, Appl
26	10	50.0	21	9	US-10-085-906-387	Sequence 387, App
27	10	50.0	21	10	US-09-901-484A-420	Sequence 420, App
c 28	10	50.0	23	9	US-10-090-887-8	Sequence 8, Appli
c 29	10	50.0	23	10	US-09-808-382-4	Sequence 4, Appli
30	10	50.0	24	9	US-09-940-185-2918	Sequence 2918, Ap
31	10	50.0	25	8	US-08-647-444-5	Sequence 5, Appli
c 32	10	50.0	25	9	US-10-098-263B-5700	Sequence 5700, Ap
33	10	50.0	25	9	US-10-098-263B-12238	Sequence 12238, A
34	10	50.0	25	9	US-10-098-263B-34264	Sequence 34264, A
c 35	10	50.0	25	9	US-10-098-263B-42033	Sequence 42033, A
c 36	10	50.0	25	9	US-10-098-263B-42034	Sequence 42034, A
c 37	10	50.0	25	9	US-10-098-263B-44063	Sequence 44063, A
c 38	10	50.0	25	9	US-10-098-263B-49892	Sequence 49892, A
39	10	50.0	25	9	US-10-098-263B-56499	Sequence 56499, A
40	10	50.0	25	9	US-10-098-263B-56500	Sequence 56500, A
41	10	50.0	25	9	US-10-098-263B-72819	Sequence 72819, A
42	10	50.0	25	9	US-10-098-263B-78124	Sequence 78124, A
c 43	10	50.0	25	9	US-10-098-263B-79153	Sequence 79153, A
c 44	10	50.0	25	9	US-10-098-263B-79154	Sequence 79154, A
45	10	50.0	25	9	US-10-098-263B-83271	Sequence 83271, A

ALIGNMENTS

RESULT 1

US-09-288-971-6/c
; Sequence 6, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288, 971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-6

Query Match 60.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
DB 28 CTGACAGAGCCC 17

RESULT 2

US-09-288-971-10
; Sequence 10, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288, 971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 10

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; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-10

Query Match      60.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
DB 4 CTGACAGAGCCC 15

RESULT 3
US-09-969-373-3187
; Sequence 3187, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3187
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3187

Query Match      55.0%; Score 11; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
DB 7 GCCCAACTCTT 17

RESULT 4
US-10-222-334-65/c
; Sequence 65, Application US/10222334
; Publication No. US20030073116A1
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Gallia
; APPLICANT: Tsal, Han-Mou
; TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
; FILE REFERENCE: UM-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/312,834
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 65
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-222-334-65

Query Match      55.0%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 11
DB 11 CTGACAGAGCCC 1

RESULT 5
US-09-940-185-2291
; Sequence 2291, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2291
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2291

Query Match      55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCC 12
DB 7 TGACAGAGCCC 17

RESULT 6
US-09-898-779-110/c
; Sequence 110, Application US/09898779
; Patent No. US20020106657A1
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Maren T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; FILE REFERENCE: 18810-82302
; CURRENT APPLICATION NUMBER: US/09/898,779
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/347,114
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-779-110

Query Match      55.0%; Score 11; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 11
DB 19 CTGACAGAGCCC 9

```

RESULT 7

US-09-992-665-205
 ; Sequence 205, Application US/09992665
 ; Publication No. US20030092009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaia Palm
 ; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ; FILE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: CEMINES.002A
 ; CURRENT APPLICATION NUMBER: US/09/992,665
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: 60/249,508
 ; PRIOR FILING DATE: 2000-11-16
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 205
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-09-992-665-205

Query Match 55.0%; Score 11; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13

Db 3 GACAGAGCCCA 13

RESULT 8

US-10-098-263B-110352
 ; Sequence 110352, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 110352
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-110352

Query Match 55.0%; Score 11; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCAACTCTTC 20

Db 3 CCCAACTCTTC 13

RESULT 9

US-09-118-276-16
 ; Sequence 16, Application US/09118276
 ; Patent No. US20010011381A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BABYCHUK, ELENA;
 ; APPLICANT: KUSHNIR, SERGEI;
 ; APPLICANT: DE BLOCK, MARC;
 ; APPLICANT: INZE, DIRK
 ; TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED
 ; CELL DEATH IN EUKARYOTIC CELLS

NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SIXBEY, FRIEDMAN, LEEDOM, & FERGUSON
 STREET: 8180 GREENSBORO DRIVE, SUITE 800
 CITY: MCLEAN,
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3-1/2" DISKETTE
 COMPUTER: IBM-COMPATIBLE
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/118,276
 FILING DATE: 17-JUL-1998
 PRIOR APPLICATION DATA: NONE
 ATTORNEY/AGENT INFORMATION:
 NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH H.
 REGISTRATION NUMBER: 31,196; 43,077
 REFERENCE/DOCKET NUMBER: 6201-0003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 790-9110
 TELEFAX: (703) 883-0370
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 BASES
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 US-09-118-276-16

Query Match 55.0%; Score 11; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCAACTCTTC 20

Db 11 CCCAACTCTTC 21

RESULT 10

US-09-824-017-24/c
 ; Sequence 24, Application US/09824017
 ; Publication No. US20020197668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BURGER, Alexander
 ; HALLER, Michael
 ; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 ; FORMULATIONS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: POLEY & LARDNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/824,017
 FILING DATE: 03-Apr-2001
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,896
 FILING DATE: 1998-02-20
 ATTORNEY/AGENT INFORMATION:
 NAME: Sandercock, Colin G.
 REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-824-017-24

Query Match 55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
| | | | | | | | | |
DB 28 GACAGAGCCCA 18

RESULT 11

US-09-986-118A-24/c
Sequence 24, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-No. US20030021806A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-986-118A-24

Query Match 55.0%; Score 11; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GACAGAGCCCA 13
| | | | | | | | | |
DB 28 GACAGAGCCCA 18

RESULT 12

US-09-824-017-25/c
Sequence 25, Application US/09824017
Publication No. US20020197669A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-824-017-25

Query Match 55.0%; Score 11; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
| | | | | | | | | |
DB 36 GACAGAGCCCA 26

RESULT 13

US-09-986-118A-25/c
Sequence 25, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY & LARDNER
;; STREET: 3000 K Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/09/986,118A
;; APPLICATION NUMBER: US/09/986,118A
;; FILING DATE: 07-NO. US20030021806A1-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/026,896
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sandercock, Colin G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37067/102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5399
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Primer"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-986-118A-25

Query Match 55.0%; Score 11; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACAGAGCCCA 13
Db 36 GACAGAGCCCA 26
RESULT 14
US-09-818-875-1383
; Sequence 1383, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1383
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-818-875-1383

Query Match 50.0%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GAGCCCAACT 16
Db 1 GAGCCCAACT 10

RESULT 15

US-09-818-875-1384/c
; Sequence 1384, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1384

Query Match 50.0%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GAGCCCAACT 16
Db 17 GAGCCCAACT 8

Search completed: June 23, 2003, 20:01:30
Job time : 160.717 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTTTC 20

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

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5: /cgn2_6/prodata/2/ina/PCTUS-COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-08-770-565-6	Sequence 6, Appli
2	20	100.0	30	US-08-770-565-5	Sequence 5, Appli
3	14	70.0	26	US-08-974-180-33	Sequence 33, Appli
4	11	55.0	15	US-08-292-620A-451	Sequence 451, App
5	11	55.0	15	US-09-071-845-451	Sequence 451, App
6	11	55.0	18	US-08-273-776-12	Sequence 12, Appl
7	11	55.0	18	US-08-255-892-42	Sequence 42, Appl
8	11	55.0	20	US-08-358-993-2	Sequence 2, Appli
9	11	55.0	20	US-08-913-547-3	Sequence 3, Appli
10	11	55.0	21	US-08-927-219-29	Sequence 29, Appl
11	11	55.0	24	US-09-347-114A-110	Sequence 110, App
12	11	55.0	36	US-08-944-368A-24	Sequence 24, Appl
13	11	55.0	36	US-09-820-764-24	Sequence 24, Appl
14	11	55.0	38	US-08-944-368A-25	Sequence 25, Appl
15	11	55.0	38	US-09-820-764-25	Sequence 25, Appl
16	11	55.0	42	US-09-051-363-23	Sequence 23, Appl
17	10	50.0	17	US-08-292-620A-1733	Sequence 1733, Ap
18	10	50.0	17	US-08-071-845-1733	Sequence 1733, Ap
19	10	50.0	17	US-08-584-040-5345	Sequence 5345, Ap
20	10	50.0	18	US-08-599-252-1	Sequence 1, Appli
21	10	50.0	18	US-08-436-074-1	Sequence 1, Appli
22	10	50.0	18	US-09-050-159-5	Sequence 5, Appli
23	10	50.0	18	PCT-US96-06352-1	Sequence 1, Appli
24	10	50.0	18	PCT-US96-06583-1	Sequence 1, Appli
25	10	50.0	20	US-08-770-565-7	Sequence 7, Appli
26	10	50.0	20	US-08-911-894-75	Sequence 75, Appl
27	10	50.0	20	US-08-338-579A-49	Sequence 49, Appl

Sequence 26, Appli
Sequence 49, Appli
Sequence 250, App
Sequence 420, App
Sequence 420, App
Sequence 24, Appli
Sequence 2, Appli
Sequence 25, Appli
Sequence 67, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 2026, Ap
Sequence 2181, Ap

ALIGNMENTS

RESULT 1
US-08-770-565-6
; Sequence 6, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2

US-08-770-565-5
 ; Sequence 5, Application US/08770565
 ; Patent No. 5846723
 ; GENERAL INFORMATION:
 ; APPLICANT: Kim, Nam Woo
 ; APPLICANT: Wu, Fred
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ronald
 ; APPLICANT: Weinrich, Scott L.
 ; TITLE OF INVENTION: Methods for Detecting the RNA Component of
 ; TITLE OF INVENTION: Telomerase
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,565
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002300US
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-770-565-5

Query Match 100.0%; Score 20; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20
 Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3

US-08-974-180-33/c
 ; Sequence 33, Application US/08974180
 ; Patent No. 6025194
 ; GENERAL INFORMATION:
 ; APPLICANT: Funk, Walter
 ; TITLE OF INVENTION: Methods for Modulating and Identifying
 ; TITLE OF INVENTION: Cellular Senescence
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Geron Corporation
 ; STREET: 230 Constitution Drive
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,180
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaster, Kevin R.
 ; REGISTRATION NUMBER: 32,704
 ; REFERENCE/DOCKET NUMBER: 206
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 473-7779
 ; TELEFAX: (650) 473-8654
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..26
 ; OTHER INFORMATION: /note= "primer hTR S328"
 ; US-08-974-180-33

Query Match 70.0%; Score 14; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAA 14
 Db 14 CTGACAGAGCCCAA 1

RESULT 4

US-08-292-620A-451
 ; Sequence 451, Application US/08292620A
 ; Patent No. 5837542
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm
 ; APPLICANT: Dan T. Stinchcomb
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Sean Sullivan
 ; APPLICANT: Kenneth G. Draper
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; TITLE OF INVENTION: DISEASES OR CONDITIONS
 ; TITLE OF INVENTION: RELATED TO LEVELS OF
 ; TITLE OF INVENTION: INTRACELLULAR ADHESION
 ; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
 ; NUMBER OF SEQUENCES: 2390
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/292,620A
 ; FILING DATE: August 17, 1994
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-451

Query Match 55.0%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 4.8e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCACTCTTC 20
Db 1 CCCACUCUC 11

RESULT 5

US-09-071-845-451
Sequence 451, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwigen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 451:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-451

Query Match 55.0%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 4.8e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCACTCTTC 20
Db 1 CCCACUCUC 11

RESULT 6

US-08-273-776-12
Sequence 12, Application US/08273776
Patent No. 5510084
GENERAL INFORMATION:
APPLICANT: Cros, Philippe
APPLICANT: Allibert, Patrice Andre
APPLICANT: Dalbon, Pascal Thierry
TITLE OF INVENTION: Process for Immobilizing a Nucleic Acid
TITLE OF INVENTION: Fragment by Passive Attachment to a Solid Substrate, the
TITLE OF INVENTION: Solid Substrate thus Obtained and Its Use.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff and Berridge
STREET: 700 S. Washington St.
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,776
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,953
FILING DATE: 17-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPE28083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-273-776-12

Query Match 55.0%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
| | | | | | | | | |
Db 4 GACAGAGCCCA 14

RESULT 7

US-08-255-892-42
; Sequence 42, Application US/08255892
; Patent No. 5695926
; GENERAL INFORMATION:
; APPLICANT: CROS, PHILIPPE
; APPLICANT: ALLIBERT, PATRICE
; APPLICANT: MALLAT, FRANCOIS
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION
; TITLE OF INVENTION: TECHNIQUE
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,892
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/834,543
; FILING DATE: 11-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DEEVER, DONALD B.
; REGISTRATION NUMBER: 23,048
; REFERENCE/DOCKET NUMBER: 1032/94109
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-255-892-42

Query Match 55.0%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
| | | | | | | | | |
Db 4 GACAGAGCCCA 14

RESULT 8

US-08-358-995-2/c
; Sequence 2, Application US/08358995

; Patent No. 5741638
; GENERAL INFORMATION:
; APPLICANT: AKIO YAMANE
; TITLE OF INVENTION: Microtiter Well For Detecting
; TITLE OF INVENTION: Nucleic Acid
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,995
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,572
; FILING DATE: January 14, 1993
; APPLICATION NUMBER: 07/722,673
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "having biotin at
; OTHER INFORMATION: 5' end with a spacer"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:

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; ISSUE:
; DATE:
; PAGES:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-358-995-2

Query Match          55.0%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
Db 18 GACAGAGCCCA 8

RESULT 9
US-08-913-547-3
; Sequence 3, Application US/08913547A
; Patent No. 6027891
; GENERAL INFORMATION:
; APPLICANT: VON KNEBEL-DOBRITZ, Magnus
; APPLICANT: WORNER, Stefano
; APPLICANT: EMERICH, Florian
; TITLE OF INVENTION: A METHOD OF EARLY DETECTION OF
; TITLE OF INVENTION: HPV-ASSOCIATED CARCINOMAS AND EXTREME DYSPLASIAS
; TITLE OF INVENTION: CAUSED BY HPV
; FILE REFERENCE: 035280028999
; CURRENT APPLICATION NUMBER: US/08/913,547A
; CURRENT FILING DATE: 1998-01-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-913-547-3

Query Match          55.0%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
Db 3 GACAGAGCCCA 13

RESULT 10
US-08-927-219-29
; Sequence 29, Application US/08927219
; Patent No. 6197533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Naohisa
; APPLICANT: Kaisaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,219
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,679
; FILING DATE: 30-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,056
; FILING DATE: 02-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,719
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-927-219-29

Query Match          55.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCC 12
Db 5 TGACAGAGCCC 15

RESULT 11
US-09-347-114A-110/c
; Sequence 110, Application US/09347114A
; Patent No. 6297014
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Maren T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; TITLE OF INVENTION: No. 6297014-responsiveness to Statin Drug Treatment
; FILE REFERENCE: P07 41878
; CURRENT APPLICATION NUMBER: US/09/347,114A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-114A-110

Query Match          55.0%; Score 11; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCC 11
Db 19 CTGACAGAGCC 9

RESULT 12

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US-08-944-368A-24/c
; Sequence 24, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-944-368A-24

Query Match 55.0%; Score 11; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GACAGAGCCCA 13
| | | | | | | | | |
Db 28 GACAGAGCCCA 18

RESULT 13
US-09-820-764-24/c
; Sequence 24, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-820-764-24

Query Match 55.0%; Score 11; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GACAGAGCCCA 13
| | | | | | | | | |
Db 28 GACAGAGCCCA 18

RESULT 14
US-08-944-368A-25/c
; Sequence 25, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-944-368A-25

Query Match 55.0%; Score 11; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 36 GACAGAGCCCA 26

RESULT 15

US-09-820-764-25/C
; Sequence 25, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLER, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO.: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-820-764-25

Query Match 55.0%; Score 11; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
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Db 36 GACAGAGCCCA 26

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Job time : 31.3147 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTCTTC 20

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Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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- 11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
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- 21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
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- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAV41173	RNA component of h
2	20	100.0	30	AAV41172	RNA component of h
3	14	70.0	26	AAV7131	PCR primer hTR S32
4	14	70.0	30	AAA61649	Mouse Elf-1 revers
5	12	60.0	20	ABL43397	Human chromosome 1
6	12	60.0	21	AAZ23852	Rye microsatellit
7	12	60.0	21	AAZ36927	S. cereale microsa
8	12	60.0	24	AAV36173	PCR primer used to
9	12	60.0	43	AAI74547	Human silent SNP c

c	10	12	60.0	46	22	AAI74549	Human silent SNP c
c	11	12	60.0	50	21	AAA40237	Construct pc2-m9#5
c	12	11	55.0	13	23	ABF03254	Oligonucleotide SE
c	13	11	55.0	13	23	ABF03255	Oligonucleotide SE
c	14	11	55.0	13	23	ABH33140	Oligonucleotide SE
c	15	11	55.0	13	23	ABH33141	Oligonucleotide SE
c	16	11	55.0	15	16	AAZ52289	Mouse ICAM hammerh
c	17	11	55.0	18	13	AAQ20414	Detection probe #2
c	18	11	55.0	18	14	AAQ36192	Detection probe fo
c	19	11	55.0	20	10	AAV97152	HPV-16 primer (694
c	20	11	55.0	20	10	AAV94234	Sequence of probe
c	21	11	55.0	20	17	AAV36613	s' primer for huma
c	22	11	55.0	20	22	AAV52648	Human diacylglycer
c	23	11	55.0	21	19	AAV52648	Hepatocyte nuclear
c	24	11	55.0	21	21	AAZ77184	Human biallelic ma
c	25	11	55.0	21	22	AAH01363	aac(3')-IIB resist
c	26	11	55.0	21	22	AAV95841	Human gene single
c	27	11	55.0	21	24	ABA91189	Collectin PCR prim
c	28	11	55.0	22	22	AAH01361	aac(3')-IIB resist
c	29	11	55.0	23	21	AAA09876	Human papillomavir
c	30	11	55.0	24	10	AAV97159	HPV probe. Synthe
c	31	11	55.0	24	10	AAV94236	Sequence of probe
c	32	11	55.0	24	22	AAV64166	Primer #106. Homo
c	33	11	55.0	24	24	ABQ02284	Oligonucleotide ad
c	34	11	55.0	24	24	ABQ08497	Oligonucleotide ad
c	35	11	55.0	24	24	ABQ08538	Oligonucleotide ad
c	36	11	55.0	25	16	AAQ87036	Oligonucleotide pr
c	37	11	55.0	25	24	ABT03684	Human NeuroD1 gene
c	38	11	55.0	26	21	AAZ60622	PCR primer used to
c	39	11	55.0	30	16	AAQ91372	PCR primer for Al.
c	40	11	55.0	36	20	AAZ23409	HPV16L1E7 fusion p
c	41	11	55.0	36	20	AAZ23421	HPV16L1E7 fusion p
c	42	11	55.0	36	20	AAZ37586	Human papilloma vi
c	43	11	55.0	36	21	AAZ48194	HPV 16 L1 expressi
c	44	11	55.0	38	20	AAZ23410	HPV16L1E7 fusion p
c	45	11	55.0	38	20	AAZ23422	HPV16L1E7 fusion p

ALIGNMENTS

RESULT 1
AAV41173
ID AAV41173 standard; DNA; 20 BP.
XX AAV41173;
XX AC
XX DT 08-OCT-1998 (first entry)
XX RNA component of human telomerase (hTR) antisense oligo 16ab.
DE DE RNA component of human telomerase; antisense oligonucleotide; infection;
KW KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW KW immune system down-regulation; anti-inflammatory therapy; ss.
XX KW
OS Synthetic.
XX OS Homo sapiens.
XX PN WO9828442-A1.
XX PD 02-JUL-1998.
XX PF 19-DEC-1997; 97WO-US23619.
XX PR 20-DEC-1996; 96US-0770565.
XX PR 20-DEC-1996; 96US-0770564.
XX PA (GERO-) GERON CORP.
XX PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX DR

XX New polynucleotide(s) antisense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
|||||
DB 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
AAV41172
ID AAV41172 standard; DNA; 30 BP.
AC AAV41172;
XX
XX 08-OCT-1998 (first entry)
DE
DE RNA component of human telomerase (hTR) antisense oligo 16.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immuno-suppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX

PT New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
|||||
DB 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
AAV77131/c
ID AAX77131 standard; DNA; 26 BP.
XX
XX AAX77131;
XX
XX 03-AUG-1999 (first entry)
XX
XX PCR primer hTR S328.
XX
XX Cellular senescence; modulator; GC6 gene; senescent gene expression;
KW pGC6; human; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO9925878-A2.
XX
XX 27-MAY-1999.
XX
XX 19-NOV-1998; 98WO-US24996.
XX
XX 19-NOV-1997; 97US-0974180.
XX
XX (GERO-) GERON CORP.
XX
XX Funk W;
XX
XX WPI; 1999-347496/29.
XX
XX New human GC6 gene, useful for identifying agents for treating
PT diseases and/or conditions associated with cell senescence
XX
XX Example 5; Page 74; 79pp; English.
XX

CC The invention relates to methods for modulating and identifying cellular
 CC senescence. Recombinant expression vectors comprising a recombinant
 CC polynucleotide corresponding to a polynucleotide in a human G6C gene, are
 CC useful for altering senescent gene expression. The vectors and host cells
 CC comprising the vectors are useful for identifying agents that prevent or
 CC modulate senescent gene expression. The polynucleotides are useful for
 CC producing the protein, pGC6 and nucleic acid derivatives. The proteins
 CC encoded are useful for raising antibodies specific for pGC6, which are
 CC useful for isolating pGC6, and for detecting cells comprising pGC6 in
 CC complex cell mixtures. The characterization of the polynucleotides enable
 CC the identification of therapeutic agents that identify and distinguish
 CC between young and senescent cells. This enables treatment of aging
 CC diseases induced or exacerbated by cellular senescence.

XX Sequence 26 BP; 1 A; 8 C; 9 G; 8 T; 0 other;

Query Match 70.0%; Score 14; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 69;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAA 14
 |||||
 DB 14 CTGACAGAGCCCAA 1

RESULT 4

AAA61649/c
 ID AAA61649 standard; DNA; 30 BP.

XX
 AC AAA61649;

DT 23-OCT-2000 (first entry)

XX Mouse Elf-1 reverse PCR primer.

XX Elf-1; mouse; transcriptional regulatory factor; rat;
 KW Polymorphic variant; immunological disease; allergic disease;
 KW PCR primer; ss.

OS Mus sp.

XX JP2000135088-A.

XX 16-MAY-2000.

XX 30-OCT-1998; 98JP-0309595.

XX 30-OCT-1998; 98JP-0309595.

XX (ASAK) ASAHI BREWERIES LTD.

XX WPI; 2000-425802/37.

XX A transcription regulating factor Elf-1 cDNA and its polymorphism -

PS Example 1; Page 4; 2ipp; Japanese.

XX The invention relates to three polymorphic variants of a rat
 CC transcriptional regulatory factor Elf-1 (AA03190-803192) and nucleic
 CC acids encoding them (AAA61645-A61647). The invention also encompasses
 CC the use of Elf-1 for regulating the transcription of a gene in an
 CC expression vector. The cDNA encoding rat Elf-1 variant #1 (AAA61645)
 CC was isolated using PCR primers (AAA61648-A61649) based on mouse Elf-1
 CC cDNA, and the rat Elf-1 variant #2 and #3 cDNAs (AAA61646-A61647) were
 CC subsequently isolated. The Elf-1 cDNA and protein sequences are
 CC potentially useful for the prevention and treatment of immunological and
 CC allergic diseases mediated by Elf-1. Sequences AAA61648-A61649 represent
 CC mouse Elf-1 PCR primers used in an exemplification of the invention to
 CC isolate rat Elf-1 variant #1 cDNA.

XX Sequence 30 BP; 9 A; 4 C; 7 G; 10 T; 0 other;

Query Match 70.0%; Score 14; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 69;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTT 19
 |||||
 DB 19 AGAGCCCAACTCTT 6

RESULT 5

ABL43397

ID ABL43397 standard; DNA; 20 BP.

XX
 AC ABL43397;

XX 11-APR-2002 (first entry)

XX Human chromosome 1p36-35 PCR primer SEQ ID NO:441.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
 KW genome; PCR primer; ss.

OS Homo sapiens.

XX JP2001321190-A.

XX 20-NOV-2001.

XX 12-MAR-2001; 2001JP-0068285.

XX 10-MAR-2000; 2000JP-0066716.

XX (RIKA) RIKAGAKU KENKYUSHO.

XX (GENO-) GENOTEX YG.

XX WPI; 2002-144136/19.

XX Arraying genome clones -

XX Claim 4; Page 13; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention.

XX Sequence 20 BP; 4 A; 8 C; 1 G; 7 T; 0 other;

Query Match 60.0%; Score 12; DB 24; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTC 20
 |||||
 DB 2 GCCCAACTCTTC 13

```

RESULT 6
AAZ23852
ID AAZ23852 standard; DNA; 21 BP.
XX AC AAZ23852;
XX
XX
XX 21-JAN-2000 (first entry)
XX
XX Rye microsatellite marker 13 PCR primer 2.
XX
XX Microsatellite marker; rye; hypervariable genomic region; Poaceae;
XX Triticeae; breeding program; DNA fingerprinting; variety; detection;
XX self pollination; cross pollination; cytoplasmic line; genetic mapping;
XX polymorphism; PCR primer; ss.
XX
XX Synthetic.
XX Secale cereale.
XX
XX DE19811506-A1.
XX
XX 21-OCT-1999.
XX
XX 17-MAR-1998; 98DE-1011506.
XX
XX 17-MAR-1998; 98DE-1011506.
XX
XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
XX WPI; 1999-591715/51.
XX
XX New microsatellite markers for rye and closely related grasses, used
XX for genetic analysis and in breeding
XX
XX Claim 6; Page 27; 28pp; German.
XX
XX This invention describes novel microsatellite markers (MSM), based on
XX the hypervariable genomic regions of rye (Secale cereale) and of plants
XX from the tribes Triticeae and Poaceae. MSM, which are new genetic markers
XX for rye and closely related species, are used for genetic analysis and
XX in breeding programs. Typical applications are in DNA fingerprinting;
XX identification of varieties; detection of self and cross pollination;
XX characterization of cytoplasmic lines, and genetic mapping (of mono- or
XX poly-genic traits). MSM show a higher degree of polymorphism than known
XX markers (both within and between different rye varieties and lines); can
XX be detected by polymerase chain reaction, so that even very small
XX samples may be analyzed, and generate many alleles per marker locus.
XX AAZ23827-223886 represent the microsatellite marker PCR primers
XX described in the method of the invention.
XX
XX Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
XX
XX Query Match 60.0%; Score 12; DB 20; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.6e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCCCAACTCTT 19
DB 1 AGCCCAACTCTT 12

RESULT 7
AAZ36927
ID AAZ36927 standard; DNA; 21 BP.
XX
XX AAZ36927;
XX
XX 02-JUL-1999 (first entry)
XX
XX S. cereale microsatellite marker PCR primer 26.
XX
XX Microsatellite; marker; PCR primer; rye; plant; Triticeae; Poaceae;
XX simple sequence repeat; SSR; sequence tag site; STS; genetic analysis;
XX DNA fingerprinting; variety identification; self fertilization;

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KW detection; cross fertilization; cytological line; gene mapping;
XX monogenic trait; polygenic trait; ss.
XX
XX Synthetic.
XX Secale cereale.
XX
XX DE19835109-A1.
XX
XX 15-APR-1999.
XX
XX 04-AUG-1998; 98DE-1035109.
XX
XX 02-OCT-1997; 97DE-1043671.
XX
XX (GVSE-) GVS GES ERWERB & VERWERTUNG LANDWIRTSCHA.
XX
XX Saal B, Wricke G;
XX
XX WPI; 1999-245522/21.
XX
XX Microsatellite markers derived from the genome of rye, useful for
XX genetic mapping as markers of monogenic or polygenic traits
XX
XX Claim 6; Page 16; 28pp; German.
XX
XX This invention describes Secale cereale microsatellite markers based on
XX hypervariable genomic segments of Secale cereale and plants of the
XX tribes Triticeae and Poaceae. The microsatellite markers comprise a simple
XX sequence repeat (SSR) marker as sequence tag site (STS), defined by two
XX specific S. cereale defined primers, of mean length 18-26 bases and
XX flanking the microsatellite sequence (MSS). Such markers are useful for
XX genetic analysis of rye, triticale and other species of the tribes
XX Triticeae and Poaceae, e.g. for DNA fingerprinting; identification of
XX varieties; detecting self or cross fertilization; studying similarity
XX and relatedness; characterization of cytological lines, or generally any
XX sort of gene mapping. Particularly, they are useful for genetic mapping
XX and marking of mono- or poly-genic traits, selection and evaluation of
XX varietal purity or checking culture stages (particularly in hybrid
XX culture methods), purity of propagative materials, success of
XX self-fertilization and required ratio of components in populations and
XX hybrids. AAX36902-X36965 represent PCR primers used in the method of the
XX invention.
XX
XX Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
XX
XX Query Match 60.0%; Score 12; DB 20; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.6e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCCCAACTCTT 19
DB 1 AGCCCAACTCTT 12

RESULT 8
AAZ36173
ID AAX36173 standard; DNA; 24 BP.
XX
XX AAX36173;
XX
XX 15-JUL-1999 (first entry)
XX
XX PCR primer used to amplify a fragment of ICAM-6 nucleic acid.
XX
XX Intercellular adhesion molecule 6; ICAM-6; drug screening; therapy;
XX intercellular adhesion; inflammatory process; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9920762-A1.
XX
XX 29-APR-1999.
XX

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PP 22-OCT-1998; 98WO-US22442.
 XX
 PR 22-OCT-1997; 97US-0955661.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Loughney K, Staunton DE, Vazeau R;
 XX
 DR WPI; 1999-288308/24.
 XX
 XX New isolated intercellular adhesion molecule-6 used for, e.g.
 PT diagnosis of inflammatory processes
 XX
 XX Example 15; Page 53; 102pp; English.
 XX
 CC The specification describes an intercellular adhesion molecule
 CC (ICAM)-6 polypeptide. The ICAM-6 polypeptides and polynucleotides
 CC can be used for drug screening and developing products for therapy
 CC involving intercellular adhesion, e.g. in inflammatory processes.
 CC The products can also be used for detection, diagnosis and the
 CC production of transgenic animals. PCR primers AAX36170-73 were used
 CC in the course of the invention.
 XX
 XX Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;
 SQ

Query Match 60.0%; Score 12; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCA 13
 DB 1 TGACAGAGCCCA 12

RESULT 9

AAI74547/c
 ID AAI74547 standard; DNA; 43 BP.
 XX
 AC AAI74547;
 XX
 XX 09-NOV-2001 (first entry)
 DT
 XX
 DE Human silent SNP containing nucleic acid SEQ:1488.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US32758.
 XX
 PR 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 XX WPI; 2001-356160/37.
 XX
 XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -
 PT
 XX Claim 1; Page 509; 2653pp; English.

AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of the
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

SQ Sequence 43 BP; 10 A; 14 C; 6 G; 13 T; 0 other;

Query Match 60.0%; Score 12; DB 22; Length 43;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 14
 DB 28 GACAGAGCCCA 17

RESULT 10
 AAI74549/c
 ID AAI74549 standard; DNA; 46 BP.
 XX
 AC AAI74549;
 XX
 XX 09-NOV-2001 (first entry)
 DT
 XX
 DE Human silent SNP containing nucleic acid SEQ:1490.

XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US32758.

PR 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

XX Claim 1; Page 509; 2653pp; English.

AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of

CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.
 XX
 SQ Sequence 46 BP; 10 A; 15 C; 6 G; 15 T; 0 other;

Query Match 60.0%; Score 12; DB 22; Length 46;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
 |||||
 Db 28 GACAGAGCCCAA 17

RESULT 11
 AAA40237
 ID AAA40237 standard; DNA; 50 BP.

XX AAA40237;

XX 02-NOV-2000 (first entry)

DE Construct pC2-m9#518 primer P-CC(4).

XX Factor VIII; light chain; LRP; gene therapy; antihemophilic; blood;
 KW low density lipoprotein receptor-related protein; coagulation disorder;
 KW thrombotic system; fibrinolytic system; primer; ss.

XX Unidentified.

XX WO200028021-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-A700272.

XX 10-NOV-1998; 98AT-0001872.

XX (BAXT) BAXTER AG.

XX Lenting PJ, Van Mourik JA, Mertens K, Pannekoek H, Turecek P;
 PI Schwarz H, Scheiflinger F;

XX WPI; 2000-376538/32.

XX New modified form of factor VIII, useful for treating hemophilia, has
 PT altered binding to low density lipoprotein-related protein, resulting
 PT in extended in vivo half-life -

XX Example XI; Page 35; 57pp; German.

XX This invention describes a novel factor VIII polypeptide (I) with factor
 CC VIII:C activity which has a modification in at least one of the A3, C1
 CC and/or C2 domains of the light chain that modifies binding affinity to
 CC low density lipoprotein receptor-related protein (LRP). Independent
 CC claims are also included for the following: (1) DNA (II) that encodes
 CC (1); (2) an expression vector containing (II); (3) transformed cells and
 CC their descendants containing (II); (4) recombinant production of (I) by
 CC culturing cells of (C); and (5) pharmaceutical composition containing a
 CC factor VIII molecule (Ia) with factor VIII:C activity plus an LRP
 CC antagonist (III). The products of the invention have antihemophilic
 CC activity. (I) has reduced affinity for LRP, a receptor involved in
 CC clearance of factor VIII from the blood. (I), optionally formulated with
 CC an antagonist of LRP, is used for treatment of coagulation disorders,
 CC specifically hemophilia A. It may also be used to treat subjects with

CC disorders of the thrombotic or fibrinolytic systems, e.g. before,
 CC during or after surgery. Nucleic acid that encodes (I) can be used
 CC similarly in gene therapy. The light chain modifications reduce clearance
 CC of factor VIII protein from the blood, resulting in longer in vivo
 CC half-life (particularly at least 90% greater than wild type) and
 CC increased stability, in vivo or in vitro. The modifications do not
 CC adversely affect procoagulant activity. This sequence represents a primer
 CC used in the construction of the plasmid pC2-m9#518 which contains the
 CC Factor VIII light chain C2 region which is described in the method of the
 CC invention.

XX Sequence 50 BP; 11 A; 16 C; 15 G; 8 T; 0 other;

Query Match 60.0%; Score 12; DB 21; Length 50;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCT 18
 |||||
 Db 31 GAGCCCAACTCT 42

RESULT 12
 ABF03254/c
 ID ABF03254 standard; DNA; 13 BP.

XX ABF03254;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 103251 for detecting SNP TSC0025831.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

XX Claim 1; SEQ ID 103251; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABH00010-ABH99989 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 other;


```

Query Match      55.0%; Score 11; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
Db 12 GCCCAACTCTT 2

RESULT 13
ABF03255
ID ABF03255 standard; DNA; 13 BP.
XX
AC ABF03255;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 103252 for detecting SNP TSC0025831.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -
Claim 1; SEQ ID 103252; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 other;

Query Match      55.0%; Score 11; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
Db 2 GCCCAACTCTT 12

RESULT 14
ABH33140/c
ID ABH33140 standard; DNA; 13 BP.
XX

```

```

AC ABH33140;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 233117 for detecting SNP TSC0000563.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -
Claim 1; SEQ ID 233117; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 other;

Query Match      55.0%; Score 11; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCCAACTCTTC 20
Db 13 CCCCAACTCTTC 3

RESULT 15
ABH33141
ID ABH33141 standard; DNA; 13 BP.
XX
AC ABH33141;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 233118 for detecting SNP TSC0000563.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

```

XX 18-OCT-2001.
 XX PD
 XX PF 06-APR-2001; 2001WO-1B00713.
 XX PR 07-APR-2000; 2000DE-1019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX PS Claim 1; SEQ ID 233118; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 other;

Query Match 55.0%; Score 11; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CCCAACTCTTC 20
 Db 1 CCCAACTCTTC 11

Search completed: June 23, 2003, 05:43:36
 Job time : 133.216 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGCCCACTCTTC 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gas:*

18: em_gas_hum:*

19: em_gas_inv:*

20: em_gas_pln:*

21: em_gas_vrt:*

22: em_gas_fun:*

23: em_gas_mam:*

24: em_gas_mus:*

25: em_gas_other:*

26: em_gas_pro:*

27: em_gas_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	46	17	AZ379320
C 2	11	55.0	21	17	AZ781467
C 3	11	55.0	22	17	AZ393281
C 4	11	55.0	24	17	AZ309564
C 5	11	55.0	47	10	BES36289
C 6	10	50.0	22	9	AI687266

7	10	50.0	23	17	AZ331549
8	10	50.0	25	9	AI647975
9	10	50.0	28	17	AZ939438
10	10	50.0	29	17	AZ412468
11	10	50.0	30	17	AZ310102
12	10	50.0	37	9	AI572041
13	10	50.0	37	12	BG423450
14	10	50.0	37	13	BI765481
15	10	50.0	37	13	BI765481
16	10	50.0	37	13	BJ063841
17	10	50.0	38	14	H45829
18	10	50.0	39	17	AZ773780
19	10	50.0	42	17	AZ616105
20	10	50.0	43	9	AI091574
21	10	50.0	44	17	AZ309736
22	10	50.0	45	9	AI309096
23	10	50.0	45	17	AZ653181
24	10	50.0	50	9	AUI04061
25	10	50.0	50	9	AUI06667
26	9	45.0	50	9	AUI06839
27	9	45.0	21	17	AZ775541
28	9	45.0	21	17	AZ466178
29	9	45.0	23	17	AZ466178
30	9	45.0	24	17	AZ852116
31	9	45.0	25	17	AZ829708
32	9	45.0	28	9	AI756191
33	9	45.0	28	17	AZ990764
34	9	45.0	28	17	BH848229
35	9	45.0	29	17	AZ804299
36	9	45.0	30	17	AZ458346
37	9	45.0	30	17	AZ486857
38	9	45.0	31	17	AZ856886
39	9	45.0	32	10	AV962684
40	9	45.0	32	14	N72637
41	9	45.0	33	17	AZ424922
42	9	45.0	33	17	BH790221
43	9	45.0	34	9	AA798808
44	9	45.0	34	14	T89869
45	9	45.0	35	9	AI801185
			36	13	BI549792

ALIGNMENTS

RESULT 1
AZ379320/c
LOCUS AZ379320 46 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0134F22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0134F22 F, DNA sequence.
ACCESSION AZ379320
VERSION AZ379320.1 GI:10493020
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 46)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0134 row: P column: 22
 Seq primer: CCGTGTAAACACAGCCGACGT
 Class: plasmid ends
 High quality sequence stop: 46.

FEATURES

source

1. .46
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M00134P22"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 6 c 16 g 19 t
 ORIGIN
 Query Match 60.0%; Score 12; DB 17; Length 46;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAAC 15
 |||||
 Db 19 ACAGAGCCCAAC 8

RESULT 2

AZ781467/c
 LOCUS AZ781467 21 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0019F23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0019F23 R, DNA sequence.

ACCESSION AZ781467
 VERSION AZ781467.1 GI:12914189
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0019 row: F column: 23
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

1. .21
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0019F23"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 2 c 12 g 5 t
 ORIGIN
 Query Match 55.0%; Score 11; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAAC 14
 |||||
 Db 11 ACAGAGCCCAAC 1

RESULT 3

AZ393281/c
 LOCUS AZ393281 22 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0156H13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0156H13 F, DNA sequence.

ACCESSION AZ393281
 VERSION AZ393281.1 GI:10508353
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0156 row: H column: 13
 Seq primer: CTTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

Source

1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0156H13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 4 a 4 c 7 g 7 t

Query Match 55.0%; Score 11; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCCA 14
 |||||
 Db 21 ACAGAGCCCCA 11

RESULT 4
 AZ309564
 LOCUS 24 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0016509F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M016509 F, DNA sequence.

ACCESSION AZ309564
 VERSION AZ309564.1 GI:10350859
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0016 row: E column: 09
 Seq primer: CTTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

Source

1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0016E09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 6 a 4 c 10 g 4 t

Query Match 55.0%; Score 11; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCCA 13
 |||||
 Db 8 GACAGAGCCCCA 18

RESULT 5
 BE536289/C
 LOCUS BE536289 47 bp mRNA linear EST 09-AUG-2000
 DEFINITION 601062681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:344989 5', mRNA sequence.

ACCESSION BE536289
 VERSION BE536289.1 GI:9764934
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 47)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM8425 row: a column: 22
 High quality sequence stop: 47.
 Location/Qualifiers

FEATURES

Source

1..47

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3448989"
/clone_lib="NIH MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/site="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 Kb. Library prepared by Life
Technologies."
BASE COUNT      6 a      21 c      10 g      10 t
ORIGIN
Query Match      55.0%; Score 11; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. NO. 1.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GACAGAGCCCA 13
|||||
Db      34 GACAGAGCCCA 24

RESULT 6
AI687266/c
LOCUS
DEFINITION
tp94d10.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2206963 3'
similar to SW:FXS8 HUMAN P98175 DXS8237E PROTEIN; contains element
MER22 repetitive element 1; mRNA sequence.
ACCESSION
AI687266
VERSION
AI687266.1 GI:4898560
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 22)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1074 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2206963"
/clone_lib="NCI CGAP Ut3"
/tissue="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/site="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.45 Kb. Life Technologies catalog #:
11541-018"
BASE COUNT      0 a      2 c      13 g      7 t
ORIGIN

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2206963"
/clone_lib="NCI CGAP Ut3"
/tissue="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/site="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.45 Kb. Life Technologies catalog #:
11541-018"
BASE COUNT      0 a      2 c      13 g      7 t
ORIGIN

Query Match      50.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. NO. 4.3e+04;

Query Match      50.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. NO. 4.4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  CAGAGCCCAA 14
|||||
Db      12 CAGAGCCCAA 3

RESULT 7
AZ331549
LOCUS
DEFINITION
IM0059K02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059K02 R, DNA sequence.
ACCESSION
AZ331549
VERSION
AZ331549.1 GI:10394350
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: K column: 02
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0059K02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      6 a      11 c      0 g      6 t
ORIGIN

Query Match      50.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. NO. 4.4e+04;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTC 20
 |||||
 Db 12 CCAACTCTTC 21

RESULT 8

AI647975/c

LOCUS

DEFINITION

AI647975 25 bp mRNA linear EST 30-APR-1999
 uk38f04.x1 Sugano mouse kidney mklia Mus musculus cDNA clone
 IMAGE:1971295.3' similar to SW.WS3_HUMAN O00399 WS-3 PROTEIN. ;,
 mRNA sequence.

ACCESSION

AI647975.1 GI:4726653

VERSION

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

REFERENCE

AUTHORS

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
 , B., Swaller, T., Gibbons, M., Pope, D., Harvey, N., Schurk, R., Ritter
 , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LILNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:988035

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

Location/Qualifiers

1..25

/organism="Mus musculus"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1971295"

/clone_lib="Sugano mouse kidney mklia"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pME18S-FL3; Site1: DralII
 (CACTGTGG); Site 2: DralII (CACTATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DralII adaptor [TGTGGCCTACTGG], digested
 and cloned into distinct DralII sites of the pME18S-FL3
 vector (5' site CACTGTGG, 3' site CACTATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5Kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTCTCTTAAAGTGG and 3' end
 primer CCACCTGCAGCTCAGACCA."

3 a 5 c 7 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.5e+04; Length 25;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

10 ACAGAGCCCA 1

11 ACAGAGCCCA 13

12 ACAGAGCCCA 1

RESULT 9

AZ939438/c

LOCUS

DEFINITION

ACCESSION

AZ939438

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: 1 column: 21

Seq primer: GTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0198121"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="female"

/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

10 a 7 c 5 g 6 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.6e+04; Length 28;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACT 16
 |||||
 Db 25 GAGCCCAACT 16

RESULT 10
 AZ412468/c
 LOCUS
 DEFINITION 29 bp DNA linear GSS 03-OCT-2000
 clone UUGC1M0185M20 R, DNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0185 row: M column: 20
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source

1..29
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0185M20"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse, DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 3 c 13 g 10 t
 ORIGIN

Query Match 50.0%; Score 10; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGCCCAACTC 17
 |||||
 Db 15 AGCCCAACTC 6

RESULT 11
 AZ310102/c
 LOCUS
 DEFINITION 30 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0018D24 R, DNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0018 row: D column: 24
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 30.

FEATURES
 source

1..30
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0018D24"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse, DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 2 a 14 c 5 g 9 t
 ORIGIN

Query Match 50.0%; Score 10; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY 1 CTGACAGAGC 10
Db 24 CTGACAGAGC 15

RESULT 12
AI572041
LOCUS
DEFINITION
tr72h02.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2223891 3'
similar to SW:PRCF HUMAN P40306 PROTEASOME COMPONENT MECL-1
PRECURSOR : mRNA sequence.
ACCESSION
AI572041
VERSION
AI572041.1 GI:4535415
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 37)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA sequencing by: Washington University Genome Sequencing Center
Cloned distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 770 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No. Location/Qualifiers
1..37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2223891"
/clone_lib="NCI CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life technologies catalog #:
11548-013"
7 a 9 c 14 g 5 t

BASE COUNT
9 a 9 c 14 g 5 t

Query Match 50.0%; Score 10; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAA 14
Db 13 CAGAGCCCAA 22

RESULT 13
BG423450
LOCUS
DEFINITION
602449304F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4587696 5',
mRNA sequence.
ACCESSION
BG423450
VERSION
BG423450.1 GI:13329956
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 37)

```

```

AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DClD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI318 row: h column: 01
High quality sequence stop: 37.
Location/Qualifiers
1..37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4587696"
/clone_lib="NIH MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
7 a 11 c 12 g 7 t

BASE COUNT
7 a 11 c 12 g 7 t

Query Match 50.0%; Score 10; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGC 10
Db 20 CTGACAGAGC 29

RESULT 14
BI765481/c
LOCUS
DEFINITION
603050546F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190683 5',
mRNA sequence.
ACCESSION
BI765481
VERSION
BI765481.1 GI:15757059
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 37)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11476 row: 1 column: 12
High quality sequence stop: 37.
Location/Qualifiers
1..37
/organism="Homo sapiens"
/db_xref="taxon:9606"

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Db 24 CCAACTCTTC 33
 Search completed: June 23, 2003, 10:10:21
 Job time : 1033.31 secs

/clone="IMAGE:5190683"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dr primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH MGC Library."

BASE COUNT 7 a 6 c 22 g 2 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 13; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCT 18
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 Db 21 GCCCAACTCT 12

RESULT 15
 BJ063841
 LOCUS
 DEFINITION 37 bp mRNA linear EST 10-DEC-2001
 laevis cDNA clone XL077114 5', mRNA sequence.

ACCESSION BJ063841
 VERSION BJ063841.1 GI:17471031
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM
 Xenopus laevis
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 37)
 AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
 ,Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tahini@genes.nig.ac.jp.

FEATURES
 source
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 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="XL077114"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud
 library"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /note="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
 were oligo-dr primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library is subtracted
 and was constructed by N. Garrett and A.M. Zorn,
 (Wellcome/CRC Institute)."
 5 a 15 c 3 g 13 t 1 others

BASE COUNT 5 a 15 c 3 g 13 t 1 others
 ORIGIN
 Query Match 50.0%; Score 10; DB 13; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 CCAACTCTTC 20

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCACTCTTC 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-08-770-565-6
2	20	100.0	30	2	US-08-770-565-5
3	14.4	72.0	42	4	US-09-051-363-23
4	14	70.0	26	3	US-08-974-180-33
5	12.8	64.0	30	4	US-08-339-214-100
6	12.6	63.0	20	4	US-09-657-452A-168
7	12.6	63.0	35	4	US-09-270-542-130
8	12.6	63.0	41	1	US-08-305-700-1
9	12.6	63.0	41	1	US-08-528-122-1
10	12.6	63.0	41	5	PCT-US95-11720-1
11	12.4	62.0	15	1	US-08-311-486C-658
12	12.4	62.0	20	3	US-09-166-186-135
13	12.4	62.0	20	4	US-09-313-932-135
14	12.4	62.0	40	4	US-09-410-903-74
15	12.4	62.0	45	1	US-08-171-389-10
16	12.4	62.0	45	1	US-08-123-936-10
17	12.4	62.0	45	2	US-08-475-228A-10
18	12.4	62.0	45	3	US-08-482-080A-10
19	12.4	62.0	45	4	US-09-354-947-10
20	12.4	62.0	45	5	PCT-US93-12388-10
21	12.2	61.0	20	1	US-08-469-802B-21
22	12.2	61.0	20	2	US-08-267-803B-39
23	12.2	61.0	20	4	US-09-467-642-63
24	12.2	61.0	31	4	US-09-648-040-1
25	12	60.0	21	1	US-08-031-143B-29
26	12	60.0	21	5	PCT-US94-02891-29
27	12	60.0	30	1	US-08-484-557C-46

c 28	12	60.0	30	1	US-08-487-426B-46	Sequence 46, Appl
c 29	12	60.0	30	2	US-08-487-720A-46	Sequence 46, Appl
c 30	12	60.0	37	1	US-08-653-740-30	Sequence 30, Appl
c 31	12	60.0	37	2	US-09-073-594-30	Sequence 30, Appl
c 32	12	60.0	37	3	US-09-275-925-30	Sequence 30, Appl
c 33	12	60.0	40	3	US-08-831-132-16	Sequence 16, Appl
c 34	12	60.0	40	4	US-09-416-150-16	Sequence 16, Appl
c 35	12	60.0	48	2	US-08-448-418-56	Sequence 56, Appl
c 36	11.8	59.0	20	2	US-08-726-012B-12	Sequence 12, Appl
c 37	11.8	59.0	20	4	US-09-487-445-141	Sequence 141, Appl
c 38	11.8	59.0	27	1	US-08-196-538-8	Sequence 8, Appl
c 39	11.8	59.0	39	3	US-08-630-820-3	Sequence 3, Appl
c 40	11.8	59.0	39	4	US-08-706-945D-24	Sequence 24, Appl
c 41	11.8	59.0	42	4	US-09-142-956B-9	Sequence 9, Appl
c 42	11.8	59.0	42	4	US-09-142-956B-9	Sequence 9, Appl
c 43	11.6	58.0	20	1	US-08-222-177A-155	Sequence 155, Appl
c 44	11.6	58.0	20	3	US-08-338-579A-49	Sequence 49, Appl
c 45	11.6	58.0	20	4	US-09-487-368A-141	Sequence 141, Appl

ALIGNMENTS

RESULT 1

US-08-770-565-6
; Sequence 6, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 0.057; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CTGACAGAGCCCACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
US-08-770-565-5
Sequence 5, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,363
FILING DATE: 07-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02906
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 8/211892 JP
FILING DATE: 23-JUL-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/012001
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
US-09-051-363-23

Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
US-09-051-363-23/c
Sequence 23, Application US/09051363
Patent No. 6270993
GENERAL INFORMATION:
APPLICANT: Shibuya, Masabumi
APPLICANT: Okamoto, Masaji
APPLICANT: Niwa, Mikio
APPLICANT: Matsumoto, Tomoe
APPLICANT: Asano, Makoto
APPLICANT: Segawa, Toshiaki
TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 230 Constitution Drive
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,180
FILING DATE: 19-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R.

Query Match 72.0%; Score 14.4; DB 4; Length 42;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 ACAGAGCCCAACTCTT 19
Db 24 ACAGAGCCCAACTCTT 9

RESULT 4
US-08-974-180-33/c
Sequence 33, Application US/08974180
Patent No. 6025194
GENERAL INFORMATION:
APPLICANT: Funk, Walter
TITLE OF INVENTION: Methods for Modulating and Identifying
TITLE OF INVENTION: Cellular Senescence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Geron Corporation
STREET: 230 Constitution Drive
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,180
FILING DATE: 19-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R.

REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 206
TELEPHONE: (650) 473-7779
TELEFAX: (650) 473-8654
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..26
OTHER INFORMATION: /note= "primer htr S328"

US-08-974-180-33

Query Match 70.0%; Score 14; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGGCCCA 14
Db 14 CTGACAGGCCCA 1

RESULT 5

US-08-339-214-100
Sequence 100, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 634833410
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
TITLE OF INVENTION: Encoding the Same
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolsach & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "sense primer 19"
ANTI-SENSE: NO

US-08-339-214-100

Query Match 64.0%; Score 12.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTTC 20
Db 10 CAAAGCCCAAGCTCTTC 25

RESULT 6

US-09-657-452A-168
Sequence 168, Application US/09657452A
Patent No. 6426188
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 1 EXPRESSION
FILE REFERENCE: RTS-0125
CURRENT APPLICATION NUMBER: US/09/657,452A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 168
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-452A-168

Query Match 63.0%; Score 12.6; DB 4; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 1 TGCCAGAGTCCAGCTCATC 19

RESULT 7

US-09-270-542-130
Sequence 130, Application US/09270542
Patent No. 6329776
GENERAL INFORMATION:
APPLICANT: Altman, Timothy
APPLICANT: Scott, James
APPLICANT: Stanton, Lawrence
TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 4198/78179
CURRENT APPLICATION NUMBER: US/09/270,542
CURRENT FILING DATE: 1999-03-17
EARLIER APPLICATION NUMBER: 09/221,222
EARLIER FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 130
LENGTH: 35
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-270-542-130

Query Match 63.0%; Score 12.6; DB 4; Length 35;
Best Local Similarity 78.9%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 10 TCAAAGAGTCCCAAGCTCTTC 28

RESULT 8

US-08-305-700-1
Sequence 1, Application US/08305700

Patent No. 5541087
GENERAL INFORMATION:
APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
TITLE OF INVENTION: PROTEINS AS IMMUNOPUSINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,700
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-305-700-1

Query Match 63.0%; Score 12.6; DB 1; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
DB 10 TAAGCGAGCCCAAACTCTC 28

RESULT 9
US-08-528-122-1
Sequence 1, Application US/08528122
Patent No. 5726044
GENERAL INFORMATION:
APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
TITLE OF INVENTION: PROTEINS AS IMMUNOPUSINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,122
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-528-122-1

Query Match 63.0%; Score 12.6; DB 1; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
DB 10 TAAGCGAGCCCAAACTCTC 28

RESULT 10
PCT-US95-11720-1
Sequence 1, Application PC/TUS9511720
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
TITLE OF INVENTION: PROTEINS AS IMMUNOPUSINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11720
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-11720-1

Query Match 63.0%; Score 12.6; DB 5; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.6e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 Db 10 TAAGCGAGCCCAACTCTTC 28

RESULT 11

US-08-311-486C-658
 ; Sequence 658, Application US/08311486C
 ; Patent No. 5811300
 ; GENERAL INFORMATION:
 ; APPLICANT: Sean Sullivan
 ; APPLICANT: Kenneth Draper
 ; APPLICANT: Kevin Kisich
 ; APPLICANT: Dan T. Stinchcomb
 ; APPLICANT: James McSwiggan
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; TITLE OF INVENTION: DISEASES OR CONDITIONS
 ; TITLE OF INVENTION: RELATED TO LEVELS OF
 ; TITLE OF INVENTION: TNF-
 ; NUMBER OF SEQUENCES: 1157
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/311,486C
 ; FILING DATE: September 23, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below:
 ; APPLICATION NUMBER: 08/008,895
 ; FILING DATE: January 19, 1993
 ; APPLICATION NUMBER: 07/989,849
 ; FILING DATE: December 7, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 209/166
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 658:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-311-486C-658

Query Match 62.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 78.6%; Pred. No. 5.8e+02;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCT 18
 Db 2 CAGAGUCCAAUCU 15

RESULT 12

US-09-166-186-135/c
 ; Sequence 135, Application US/09166186A
 ; Patent No. 6080580
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Brenda
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Butler, Madeline M.
 ; APPLICANT: Shanahan, William R.
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
 ; FILE REFERENCE: ISPH-0322
 ; CURRENT APPLICATION NUMBER: US/09/166,186A
 ; CURRENT FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 250
 ; SEQ ID NO 135
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: antisense sequence
 ; US-09-166-186-135

Query Match 62.0%; Score 12.4; DB 3; Length 20;
 Best Local Similarity 92.9%; Pred. No. 6.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCT 18
 Db 17 CAGAGTCCCAACTCT 4

RESULT 13

US-09-313-932-135/c
 ; Sequence 135, Application US/09313932A
 ; Patent No. 6228642
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Brenda
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Butler, Madeline M.
 ; APPLICANT: Shanahan, William R.
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
 ; FILE REFERENCE: ISPH-0356
 ; CURRENT APPLICATION NUMBER: US/09/313,932A
 ; CURRENT FILING DATE: 1999-05-18
 ; NUMBER OF SEQ ID NOS: 501
 ; SEQ ID NO 135
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-09-313-932-135

Query Match 62.0%; Score 12.4; DB 4; Length 20;
 Best Local Similarity 92.9%; Pred. No. 6.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCT 18
 Db 17 CAGAGTCCCAACTCT 4

RESULT 14

US-09-410-903-74/c
 ; Sequence 74, Application US/09410903
 ; Patent No. 6420113
 ; GENERAL INFORMATION:
 ; APPLICANT: Buechler, Joe
 ; APPLICANT: Valkirs, Gunars
 ; APPLICANT: Gray, Jeff
 ; APPLICANT: Biosite Diagnostics Inc.
 ; TITLE OF INVENTION: Chimeric Polyclonal Antibodies
 ; FILE REFERENCE: 014907-002700US

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; CURRENT APPLICATION NUMBER: US/09/410,903
; CURRENT FILING DATE: 1999-10-02
; PRIOR APPLICATION NUMBER: US 08/832,985
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: US 08/835,159
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: WO PCT/US98/06704
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide 3' PCR primer 876
US-09-410-903-74

Query Match          62.0%; Score 12.4; DB 4; Length 43;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CAGAGCCCAACTCT 18
      |||||
Db      32 CAGAGCCCAACTCT 19

RESULT 15
US-08-171-389-10
; Sequence 10, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,389
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE-TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; TYPE: DNA
; INDIVIDUAL ISOLATE: Human gene fragment for the
; INDIVIDUAL ISOLATE: acetylcholine receptor gamma
US-08-171-389-10

Query Match          62.0%; Score 12.4; DB 1; Length 45;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CAGAGCCCAACTCT 18
      |||||
Db      32 CAGAGCCCAACTCT 45

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Job time : 31.3586 secs
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20
Sequence: 1 CTGACAGAGCCCAACTCTTC 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	72.0	19	9	US-10-093-958-22
2	13.6	68.0	28	9	US-10-151-320-25
3	13.6	68.0	28	9	US-10-152-363A-48
4	13.6	68.0	29	9	US-10-152-363A-41
5	13.6	68.0	29	9	US-10-152-363A-42
6	13.6	68.0	48	9	US-10-152-363A-16
7	13.4	67.0	21	9	US-09-909-567B-23
8	13.4	67.0	33	9	US-10-006-591-8
9	13.4	67.0	35	9	US-10-216-484-86
10	13.2	66.0	25	9	US-10-098-263B-39849
11	13.2	66.0	25	9	US-10-098-263B-57306
12	13.2	66.0	28	9	US-10-152-363A-46
13	13.2	66.0	30	9	US-10-152-363A-43
14	13.2	66.0	31	9	US-10-152-363A-44
15	13.2	66.0	30	9	US-09-874-503-31
16	13.2	66.0	50	9	US-10-000-157-31
17	13.2	66.0	50	9	US-09-747-259-31
18	13.2	66.0	50	9	US-09-908-821-31
19	12.8	64.0	25	9	US-10-098-263B-2034

20	12.8	64.0	36	9	US-10-008-063-39	Sequence 39, Appl
21	12.8	64.0	36	10	US-09-375-924C-9	Sequence 9, Appl
c 22	12.6	63.0	36	9	US-10-218-547-53	Sequence 53, Appl
c 23	12.6	63.0	36	9	US-10-218-547-55	Sequence 55, Appl
c 24	12.6	63.0	49	9	US-10-006-009-4	Sequence 4, Appl
c 25	12.4	62.0	20	9	US-09-824-322B-135	Sequence 135, Appl
c 26	12.4	62.0	31	9	US-09-288-971-6	Sequence 6, Appl
c 27	12.4	62.0	31	9	US-09-288-971-10	Sequence 10, Appl
28	12.4	62.0	31	10	US-09-801-274-1303	Sequence 1303, Ap
29	12.4	62.0	36	9	US-10-008-063-29	Sequence 29, Appl
30	12.4	62.0	36	9	US-10-152-363A-19	Sequence 19, Appl
c 31	12.4	62.0	43	9	US-09-453-234-27	Sequence 27, Appl
c 32	12.4	62.0	43	9	US-10-193-960-74	Sequence 74, Appl
c 33	12.2	61.0	17	9	US-09-930-423-1249	Sequence 1249, Ap
c 34	12.2	61.0	17	9	US-09-930-423-1614	Sequence 1614, Ap
c 35	12.2	61.0	18	10	US-09-969-373-1891	Sequence 1891, Ap
c 36	12.2	61.0	22	9	US-09-791-389-304	Sequence 304, App
c 37	12.2	61.0	22	9	US-09-791-393-304	Sequence 304, App
c 38	12.2	61.0	22	10	US-09-791-378-662	Sequence 662, App
c 39	12.2	61.0	22	10	US-09-791-378-670	Sequence 670, App
40	12.2	61.0	25	9	US-10-098-263B-47598	Sequence 47598, A
41	12.2	61.0	25	9	US-10-098-263B-65640	Sequence 65640, A
42	12.2	61.0	25	9	US-10-098-263B-112540	Sequence 112540,
c 43	12.2	61.0	30	9	US-09-977-418-78	Sequence 78, Appl
c 44	12.2	61.0	30	9	US-09-977-033A-78	Sequence 1, Appl
45	12.2	61.0	31	9	US-10-217-914-1	

ALIGNMENTS

RESULT 1
US-10-093-958-22
; Sequence 22, Application US/10093958
; Publication No. US2003004423A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
; FILE REFERENCE: LEX-016
; CURRENT APPLICATION NUMBER: US/10/093,958
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,096
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: forward primer for gamma 1 hinge region
US-10-093-958-22

Query Match 72.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
Db 4 CAGAGCCCAACTCTTC 19

RESULT 2
US-10-151-320-25
; Sequence 25, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436

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; CURRENT APPLICATION NUMBER: US/10/151,320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer used for PCR.
US-10-151-320-25

Query Match      68.0%; Score 13.6; DB 9; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGGCCAGCCCAACTCTTC 20

RESULT 3
US-10-152-363A-48
; Sequence 48, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-10-152-363A-48

Query Match      68.0%; Score 13.6; DB 9; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 4 CTCAGGAGCCCAACTCTTC 23

RESULT 4
US-10-152-363A-41/c
; Sequence 41, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:

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; OTHER INFORMATION: PCR primer.
US-10-152-363A-41

Query Match      68.0%; Score 13.6; DB 9; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 21 CTCAGGAGCCCAACTCTTC 2

RESULT 5
US-10-152-363A-42
; Sequence 42, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-10-152-363A-42

Query Match      68.0%; Score 13.6; DB 9; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 9 CTCAGGAGCCCAACTCTTC 28

RESULT 6
US-10-152-363A-16/c
; Sequence 16, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-10-152-363A-16

Query Match      68.0%; Score 13.6; DB 9; Length 48;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20

```

Db 39 CTGAAGGAGCCCAACTCTTC 20

RESULT 7

US-09-909-567B-23
; Sequence 23, Application US/09909567B
; Publication No. US20030022257A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-909-567B-23

Query Match 67.0%; Score 13.4; DB 9; Length 21;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTT 19
|||||
Db 2 CAGAGCCCAACTCTT 16
|||||

RESULT 8

US-10-006-591-8/c
; Sequence 8, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GENES
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description for Artificial Sequence: primer
US-10-006-591-8

Query Match 67.0%; Score 13.4; DB 9; Length 33;
Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTT 19
|||||
Db 23 CAGAGCCCAACTCTT 9
|||||

RESULT 9

US-10-216-484-86
; Sequence 86, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 86
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain
US-10-216-484-86

Query Match 67.0%; Score 13.4; DB 9; Length 35;
Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAGAGCCCAACTCTT 19
|||||
Db 7 CAGAGCCCAACTCTT 21
|||||

RESULT 10

US-10-098-263B-39849
; Sequence 39849, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 39849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-39849

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GACAGGCCCAACTCTTC 20
|||||
Db 8 GACAGGACCTATTCTTC 25
|||||

RESULT 11

US-10-098-263B-57306/c
; Sequence 57306, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael

```

; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA

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; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-874-503-31
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	Query Match	66.0%;	Score 13.2;	DB 9;	Length 50;
	Best Local Similarity	83.3%;	Pred. No. 2.3e+03;		
	Matches 15;	Conservative 0;	Mismatches 3;	Indels	
Qy	3	GACAGAGCCCAACTCTTC	20		
Dd	46	GGCAGAGCACAACTGTTT	29		

Search completed: June 25, 2003, 22:25:04
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1697.05 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-6

Perfect score: 20

Sequence: 1 CTGACAGAGCCCAACTTTC 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA Main:*

- 1: /cgn2_6/ptodata/2/pna/pna/PCTUS COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/pna/US06 COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/pna/US07 COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/pna/US08 COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/pna/US081 COMB.seq.*
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- 24: /cgn2_6/ptodata/2/pna/pna/US096B COMB.seq.*
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- 26: /cgn2_6/ptodata/2/pna/pna/US096D COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	PCT-US97-23619-6
2	20	100.0	20	11	US-08-770-564A-6
3	20	100.0	30	1	PCT-US97-23619-5
4	20	100.0	30	11	US-08-770-564A-5
c	5	18	90.0	24	9 US-08-521-634-15
6	15.8	79.0	25	17	US-09-396-196F-124326
7	15.8	79.0	25	17	US-09-396-196G-124326
8	14.8	74.0	25	79	US-60-353-987-992959
9	14.4	72.0	19	1	PCT-US02-07011-22
10	14.4	72.0	19	39	US-10-093-958-22
c	11	14.2	71.0	25	17 US-09-396-196F-9984
12	14.2	71.0	25	17	US-09-396-196G-9984
13	14.2	71.0	25	26	US-09-660-420-102700
14	14.2	71.0	25	36	US-09-954-427-80617
15	14.2	71.0	25	36	US-09-954-427-304491
16	14.2	71.0	25	67	US-60-233-166-80617
17	14.2	71.0	25	67	US-60-233-166-304491
c	18	14.2	71.0	25	79 US-60-353-987-592670
19	14.2	71.0	25	79	US-60-353-987-736046
c	20	14.2	71.0	25	79 US-60-353-987-870013
21	14.2	71.0	47	18	US-09-422-978-3806

Sequence 5017, Ap
Sequence 119131, A
Sequence 119131, A
Sequence 66821, A
Sequence 66822, A
Sequence 66827, A
Sequence 394270, A
Sequence 97310, A
Sequence 394270, A
Sequence 738193, A
Sequence 3, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 7, Appli
Sequence 70908, A
Sequence 160140, A
Sequence 271024, A
Sequence 143419, A
Sequence 67313, A
Sequence 160140, A
Sequence 271024, A
Sequence 161404, A
Sequence 527778, A
Sequence 25, Appli

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="oligo 16ab"
PCT-US97-23619-6

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2

US-08-770-564A-6
Sequence 6, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-6

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3

PCT-US97-23619-5

ALIGNMENTS

RESULT 1
PCT-US97-23619-6
Sequence 6, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

Sequence 5, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..30
OTHER INFORMATION: /note= "oligo 16"
PCT-US97-23619-5
Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20
RESULT 4
US-08-770-564A-5
Sequence 5, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-5
Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20
RESULT 5
US-08-521-634-15/c
Sequence 15, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/330,123
 ; FILING DATE: 27-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 7-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dunn, Tracy J.
 ; REGISTRATION NUMBER: 34,587
 ; REFERENCE/DOCKET NUMBER: 15389-000850
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (oligonucleotide)
 ; US-08-521-634-15

Query Match 90.0%; Score 18; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTC 20
 DB 24 GACAGAGCCCAACTCTTC 7

RESULT 6

US-09-396-196F-124326
 ; Sequence 124326, Application US/09396196F
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196F
 ; CURRENT FILING DATE: 2001-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 124326
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 ; US-09-396-196F-124326

Query Match 79.0%; Score 15.8; DB 17; Length 25;
 Best Local Similarity 89.5%; Pred. No. 2.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 DB 2 TGACAGAGCCCAACTCTTC 20

RESULT 7

US-09-396-196G-124326
 ; Sequence 124326, Application US/09396196G
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 124326
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 ; US-09-396-196G-124326

Query Match 79.0%; Score 15.8; DB 17; Length 25;
 Best Local Similarity 89.5%; Pred. No. 2.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 DB 2 TGACAGAGCCCAACTCTTC 20

RESULT 8

US-60-353-987-992959
 ; Sequence 992959, Application US/60353987
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/60/353,987
 ; CURRENT FILING DATE: 2002-02-01
 ; NUMBER OF SEQ ID NOS: 997516
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 992959
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-60-353-987-992959

Query Match 74.0%; Score 14.8; DB 79; Length 25;
 Best Local Similarity 88.9%; Pred. No. 8.4e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTT 19
 DB 4 TGACAGAGCCCAACTCTT 21

RESULT 9

PCT-US02-07011-22
 ; Sequence 22, Application PC/TUS0207011
 ; GENERAL INFORMATION:
 ; APPLICANT: Lexigen Pharmaceuticals Corp.
 ; APPLICANT: Gillies, Stephen
 ; APPLICANT: Way, Jeffrey
 ; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
 ; TITLE OF INVENTION: Mesity
 ; FILE REFERENCE: LEX-016PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/07011
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 60/274,096
 ; PRIOR FILING DATE: 2001-03-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: forward primer for gamma 1 hinge region
 ; PCT-US02-07011-22

Query Match 72.0%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
|||||
Db 4 CAGAGCCCAACTCTTC 19

RESULT 10
US-10-093-958-22
; Sequence 22, Application US/10093958
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Jeffrey, Way
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype A
; TITLE OF INVENTION: Moiety
; FILE REFERENCE: LEX-016
; CURRENT APPLICATION NUMBER: US/10/093,958
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,096
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: forward primer for gamma 1 hinge region
US-10-093-958-22

Query Match 72.0%; Score 14.4; DB 39; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
|||||
Db 4 CAGAGCCCAACTCTTC 19

RESULT 11
US-09-396-196F-9984/c
; Sequence 9984, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9984
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196F-9984

Query Match 71.0%; Score 14.2; DB 17; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
|||||
Db 20 TGCCAGAGCCCAACATC 2

RESULT 12
US-09-396-196G-9984/c
; Sequence 9984, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9984
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-9984

Query Match 71.0%; Score 14.2; DB 17; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
|||||
Db 20 TGCCAGAGCCCAACATC 2

RESULT 13
US-09-660-220-102700
; Sequence 102700, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U73824
US-09-660-220-102700

Query Match 71.0%; Score 14.2; DB 26; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTT 19
|||||
Db 5 CTGACGAGAGCAGCAACTCTT 23

RESULT 14
US-09-954-427-80617
; Sequence 80617, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80617
; LENGTH: 25
; TYPE: DNA

```

; ORGANISM: Rattus norvegicus
;
; PUBLICATION INFORMATION:
;
; DATABASE ACCESSION NUMBER: GenBank AA819663
US-09-954-427-80617

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Query Match	71.08;	Score 14.2;	DB 36;	Length 25;
Best Local Similarity	84.2;	Prod. NO. 1.7e-04;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	CTGACAGAGCCCACTCTT	19	
Db	6	CTGACGGAGCGCACTCTT	24	

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RESULT 15
US-09-954-427-304491
; Sequence 304491, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304491
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D13966
US-09-954-427-304491

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```

Query Match      71.0%; Score 14.2; DB 36; Length 25;
Best Local Similarity 84.2%; Pred.No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 CTGACAGAGCCCACTCTT 19
          |||||
Db       1 CTAACAGACCCCTACTCTT 19
          |||||

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Search completed: June 25, 2003, 06:20:24
Job time : 1698.67 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-6
Perfect score: 20
Sequence: 1 CTGACAGAGCCCACTTTC 20

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New:*

- 1: /cgn2_6/ptodata/1/pna/US06_PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	23	1	PCT-US03-04088-522
C 2	19	95.0	21	1	PCT-US03-04088-522
C 3	19	95.0	21	1	PCT-US03-04088-544
C 4	19	95.0	21	1	PCT-US03-04088-548
C 5	19	95.0	21	1	PCT-US03-04088-552
C 6	19	95.0	21	1	PCT-US03-04088-556
C 7	19	95.0	21	1	PCT-US03-04088-560
C 8	18	90.0	19	1	PCT-US03-04088-23
C 9	18	90.0	19	1	PCT-US03-04088-287
C 10	15.8	79.0	25	12	US-60-427-808-503841
C 11	14.8	74.0	25	9	US-10-355-577-992959
C 12	14.8	74.0	25	12	US-60-427-808-449334
C 13	14.8	74.0	25	12	US-60-427-836-142384
C 14	14.8	74.0	25	12	US-60-427-836-603511
C 15	14.4	72.0	25	12	US-60-427-836-166946
C 16	14.4	72.0	25	12	US-60-427-836-359518
C 17	14.2	71.0	25	6	US-09-660-222-102700
C 18	14.2	71.0	25	9	US-10-355-577-592670
C 19	14.2	71.0	25	9	US-10-355-577-736046
C 20	14.2	71.0	25	9	US-10-355-577-870013

C 21	14.2	71.0	25	12	US-60-427-808-420907	Sequence 420907,
C 22	14.2	71.0	25	12	US-60-427-808-423385	Sequence 423385,
C 23	14.2	71.0	25	12	US-60-427-808-467623	Sequence 467623,
C 24	14.2	71.0	25	12	US-60-427-808-503840	Sequence 503840,
C 25	14.2	71.0	25	12	US-60-427-808-764602	Sequence 764602,
C 26	14.2	71.0	47	9	US-10-349-143-3806	Sequence 3806, Ap
C 27	14	70.0	25	12	US-60-427-808-47221	Sequence 47221, A
C 28	14	70.0	25	12	US-60-427-808-699316	Sequence 699316,
C 29	14	70.0	25	12	US-60-427-836-529892	Sequence 529892,
C 30	13.8	69.0	20	10	US-10-289-762-5017	Sequence 5017, Ap
C 31	13.8	69.0	25	6	US-09-660-222-66821	Sequence 66821, A
C 32	13.8	69.0	25	6	US-09-660-222-66822	Sequence 66822, A
C 33	13.8	69.0	25	6	US-09-660-222-66827	Sequence 66827, A
C 34	13.8	69.0	25	7	US-09-953-570-97309	Sequence 97309, A
C 35	13.8	69.0	25	9	US-10-355-577-738193	Sequence 738193,
C 36	13.8	69.0	25	12	US-60-427-808-99506	Sequence 99506, A
C 37	13.8	69.0	25	12	US-60-427-808-104960	Sequence 104960,
C 38	13.8	69.0	25	12	US-60-427-808-263712	Sequence 263712,
C 39	13.8	69.0	25	12	US-60-427-808-317845	Sequence 317845,
C 40	13.8	69.0	25	12	US-60-427-808-461772	Sequence 461772,
C 41	13.8	69.0	25	12	US-60-427-808-589800	Sequence 589800,
C 42	13.8	69.0	25	12	US-60-427-836-258	Sequence 258, App
C 43	13.8	69.0	25	12	US-60-427-836-78476	Sequence 78476, A
C 44	13.8	69.0	25	12	US-60-427-836-316656	Sequence 316656,
C 45	13.6	68.0	23	10	US-10-372-730-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggan, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 100.0%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
 Db 22 CTGACAGAGCCCAACTCTTC 3

RESULT 2
 PCT-US03-04088-540/c
 ; Sequence 540, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 540
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-540

Query Match 95.0%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 Db 19 TGACAGAGCCCAACTCTTC 1

RESULT 3
 PCT-US03-04088-544
 ; Sequence 544, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 544
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-544

Query Match 95.0%; Score 19; DB 1; Length 21;
 Best Local Similarity 78.9%; Pred. No. 11;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
 Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 4
 PCT-US03-04088-548/c
 ; Sequence 548, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 548
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1)

```
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

```
Query Match          95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGACAGAGCCCAACTCTTC 20
      |||||
Db      19 TGACAGAGCCCAACTCTTC 1
```

```
RESULT 5
PCT-US03-04088-552
Sequence 552, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 552
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

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FEATURE:
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
```

```
Query Match          95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGACAGAGCCCAACTCTTC 20
      |||||
Db      1 UGACAGAGCCCAACUCUC 19
```

```
RESULT 6
PCT-US03-04088-556/c
Sequence 556, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 556
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(6)
OTHER INFORMATION: 2'-deoxy
```

```

; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-556

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Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 TGACAGAGCCCACTCTTC 20
Db 19 TGACAGAGCCCACTCTTC 1

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RESULT 7
PCT-US03-04088-560
; Sequence 560, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129

```

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; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 560
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(8)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-560

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Query Match 95.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 2 TGACAGAGCCCACTCTTC 20
Db 1 UGACAGAGCCCACTCTTC 19

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```

RESULT 8
PCT-US03-04088-23/c
; Sequence 23, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20

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PCT-US03-04088-287
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
OTHER INFORMATION: region
PCT-US03-04088-23

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAACTCT 18
DB 18 CTGACAGAGCCCAACTCT 1

RESULT 9
PCT-US03-04088-287
Sequence 287, Application PC/ITUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 287
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
OTHER INFORMATION: region
PCT-US03-04088-287

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 34;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCAACTCT 18
DB 2 CUGACAGAGCCCAACUCU 19

RESULT 10
US-60-427-808-503841
Sequence 503841, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 503841
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-503841

Query Match 79.0%; Score 15.8; DB 12; Length 25;
Best Local Similarity 89.5%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACAGAGCCCAACTCTTC 20
DB 6 TGACAGAGCCCAAGTCCTC 24

RESULT 11
US-10-355-577-992959
Sequence 992959, Application US/103555577
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 992959
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-355-577-992959

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGACAGAGCCCAACTCTT 19
DB 4 TGACAGAGCCCAACTCTT 21

RESULT 12
US-60-427-808-449334
Sequence 449334, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 449334
LENGTH: 25
TYPE: DNA

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; ORGANISM: Mus musculus
US-60-427-808-449334

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTC 20
   ||||| ||||| |||||
Db 1 GACAGTGTCCAACTCTTC 18

RESULT 13
US-60-427-836-142384
; Sequence 142384, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 142384
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-142384

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTC 20
   ||||| ||||| |||||
Db 7 GACTGAGCCCACTCTTC 24

RESULT 14
US-60-427-836-603511/c
; Sequence 603511, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 603511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-603511

Query Match          74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTC 20
   ||||| ||||| |||||
Db 19 GACAGAGACCAAGTCTTC 2

RESULT 15
US-60-427-836-166946/c
; Sequence 166946, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 166946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-166946

Query Match          72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACT 16
   ||||| ||||| |||||
Db 16 CTGACAGTGCCTCAACT 1

Search completed: June 26, 2003, 04:15:15
Job time : 479.077 secs
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AR063829 30 bp DNA linear PAT 29-SEP-1999

Sequence 5 from patent US 5846723.

AR063829 1 GI:5993137

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 30)

Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.

Methods for detecting the RNA component of telomerase

Patent: US 5846723-A 5 08-DEC-1998;

Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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source
1. .30
/organism="unknown"
BASE COUNT      6 a   10 c   9 g   5 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 30; DB 6; Length 30;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30
        |||||
Db      1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30

RESULT 2
AR063830
LOCUS      AR063830      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5846723.
ACCESSION AR063830
VERSION    AR063830.1 GI:5993138
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 6 08-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="unknown"
BASE COUNT      5 a   8 c   3 g   4 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTC 20
        |||||
Db      1 CTGACAGAGCCCAACTCTTC 20

RESULT 3
AR063831
LOCUS      AR063831      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5846723.
ACCESSION AR063831
VERSION    AR063831.1 GI:5993139
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 7 08-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="unknown"
BASE COUNT      3 a   7 c   6 g   4 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCAACTCTTCGGGTGGCAG 30
        |||||
Db      1 CCAACTCTTCGGGTGGCAG 20

RESULT 4

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128704
LOCUS      I28704      46 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5573924.
ACCESSION I28704
VERSION    I28704.1 GI:1819480
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 46)
AUTHORS    Beckmann,M.Patricia., Goodwin,R.G., Giri,J.G. and Armitage,R.J.
TITLE      CD27 ligand
JOURNAL    Patent: US 5573924-A 7 12-NOV-1996;
FEATURES   Location/Qualifiers
            source
            1. .46
            /organism="unknown"
BASE COUNT      6 a   12 c   14 g   14 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 13; DB 6; Length 46;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 AACTCTTCGGGT 25
        |||||
Db      25 AACTCTTCGGGT 37

RESULT 5
AB069038
LOCUS      AB069038      20 bp      DNA      linear      SYN 08-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS sts-A008044
            at lp36.
ACCESSION AB069038
VERSION    AB069038.1 GI:15129842
KEYWORDS
SOURCE     synthetic construct DNA.
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
TITLE      A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 7p35-p36
JOURNAL    Genomics 74 (1), 55-70 (2001)
REFERENCE  2 (bases 1 to 20)
AUTHORS    Horii,A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES   Location/Qualifiers
            source
            1. .20
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            misc_feature
            1. .20
            /note="forward primer for human STS sts-A008044 at lp36
            sts-A008044 obtained from clones B316C6, B132G19, B375M9,
            Human BAC library RPCI-11"
BASE COUNT      4 a   8 c   1 g   7 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 12; DB 12; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCCCAACTCTTC 20
        |||||
Db      2 GCCCAACTCTTC 13

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manuscript"
/codon_start=2
/product="T cell receptor gamma chain"
/protein_id="AAB20598.2"
/db_xref="GI:7717239"
/translation="PLWERELG"

BASE COUNT      5 a      4 c      13 g      6 t
ORIGIN
Query Match      40.0%; Score 12; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCCCAACTCTTC 20
      |||||
Db      28 GCCCAACTCTTC 17

RESULT 8
HSTCRGV33/c
LOCUS      H. sapiens mRNA for rearranged TCR-gamma chain V region (VJ).
DEFINITION
ACCESSION      X69253
VERSION      X69253.1 GI:510639
KEYWORDS      J-region; N-region; T-cell receptor; T-cell receptor gamma chain;
              V-region.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Hvas,J.
TITLE      Direct Submission
JOURNAL      Submitted (10-JUN-1992) J. Hvas, La Trobe University,
              Neuroimmunology Lab., Dept. of Psych., La Trobe University,
              Bundoora, Victoria 3083, AUSTRALIA
              2 (bases 1 to 30)
REFERENCE
AUTHORS      Hvas,J., Oksenberg,J.R., Fernando,R., Steinman,L. and Bernard,C.C.
TITLE      Gamma delta T cell receptor repertoire in brain lesions of patients
              with multiple sclerosis
JOURNAL      J. Neuroimmunol. 46 (1-2), 225-234 (1993)
MEDLINE      93367035
PubMed      8395544
FEATURES
      source
      1..30
      /organism="Homo sapiens"
      /isolate="MS patient SEL"
      /db_xref="taxon:9606"
      /clone="MSSELBRAS5G"
      /tissue_type="brain"
      misc_feature      1..11
      /note="V-gamma-2 segment"
      misc_feature      12..16
      /note="N region"
      misc_feature      17..30
      /note="J-gamma-1.2 segment"
BASE COUNT      8 a      4 c      12 g      6 t
ORIGIN
Query Match      40.0%; Score 12; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCCCAACTCTTC 20
      |||||
Db      27 GCCCAACTCTTC 16

RESULT 9
AX158160/c
LOCUS      AX158160
DEFINITION      Sequence 1488 from Patent WO0140521.
ACCESSION      AX158160

```

```

VERSION AX158160.1 GI:14539491
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 43)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
JOURNAL Patent: WO 0140521-A 1488 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 18..19
Accession number CG29694531"
misc_feature 19
/note="Nucleotide deleted between bases 18 and 19
BASE COUNT 10 a 14 c 6 g 13 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
|||||
Db 28 GACAGAGCCCAA 17

RESULT 10
AX158162/c
LOCUS AX158162 46 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1490 from Patent WO0140521.
ACCESSION AX158162
VERSION AX158162.1 GI:14539493
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 46)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
JOURNAL Patent: WO 0140521-A 1490 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 21..22
Accession number CG29694531"
misc_feature 22
/note="Nucleotide deleted between bases 21 and 22
BASE COUNT 10 a 15 c 6 g 15 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
|||||
Db 28 GACAGAGCCCAA 17

RESULT 11
AX024597
LOCUS AX024597 50 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 13 from Patent WO028021.
ACCESSION AX024597
VERSION AX024597.1 GI:10184737
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 50)
AUTHORS Turecek,P., Scheiflinger,F., Schwarz,H.P., Lenting,P.J., van
Mourik,J.A., Pannekoek,H. and Mertens,K.
TITLE A factor viii-polypeptide with factor viii:c-activity
JOURNAL Patent: WO 0028021-A 13 18-MAY-2000;
BAXTER AKTIEGESELLSCHAFT (AT) ; TURECEK PETER (AT) ; SCHEIFLINGER
FRIEDRICH (AT) ; SCHWARZ HANS PETER (AT) ; LENTING PETRUS JOHANNES
(NL) ; MOURIK JAN AART VAN (NL) ; PANNEKOEK HANS (NL) ; MERTENS
KOENRAAD (NL)
FEATURES
source Location/Qualifiers
1. .50
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 11 a 16 c 15 g 8 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCT 18
|||||
Db 31 GAGCCCAACTCT 42

RESULT 12
AX14857/c
LOCUS AX14857 12 bp DNA linear PAT 16-MAY-1994
DEFINITION Nucleotide sequence 1 from patent number EP0334694.
ACCESSION AX14857
VERSION AX14857.1 GI:512100
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cravador,A., De Vos-Pierreux,M.J. and Bollen,A.
TITLE Nucleic acid probes with non-radioactive labels, and preparation
METHODS processes
JOURNAL Patent: EP 0334694-A 1 27-SEP-1989;
IRE-CELLTARG S.A.; LA REGION WALLONNE
FEATURES
source Location/Qualifiers
1. .12
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 0 a 4 c 4 g 4 t
ORIGIN
Query Match 36.7%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
|||||
Db 11 GACAGAGCCCA 1

RESULT 13
AR056247
LOCUS AR056247 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 451 from patent US 5837542.
ACCESSION AR056247
VERSION AR056247.1 GI:5981824
KEYWORDS

```

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 451 17-NOV-1998;
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unknown"
BASE COUNT   3 a      6 c      1 g      5 t
ORIGIN

Query Match      36.7%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCCAACTCTTC 20
Db      1 CCCAACTCTTC 11

RESULT 14
AR114005
LOCUS      AR114005      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 451 from patent US 6132967.
ACCESSION AR114005
VERSION   AR114005.1 GI:14094327
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
JOURNAL   Patent: US 6132967-A 451 17-OCT-2000;
FEATURES  Location/Qualifiers
            source
            1..15
            /organism="unknown"
BASE COUNT   3 a      6 c      1 g      5 t
ORIGIN

Query Match      36.7%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCCAACTCTTC 20
Db      1 CCCAACTCTTC 11

RESULT 15
A32455
LOCUS      A32455      18 bp      DNA      linear      PAT 07-MAY-1996
DEFINITION Synthetic papillomavirus type 16 E7 probe.
ACCESSION A32455
VERSION   A32455.1 GI:1567446
KEYWORDS
SOURCE    synthetic construct.
            synthetic construct
            artificial sequences.
            1 (bases 1 to 18)
REFERENCE 1 (bases 1 to 18)
AUTHORS   Cross,P., Allibert,P.A., Mandrand,B.F. and Dalbon,P.T.
TITLE     Method for immobilizing a nucleic acid fragment by passive
            adsorption on a solid support, solid support obtained therefrom and
            its utilisation
JOURNAL   Patent: EP 0524864-A 10 27-JAN-1993;
            BIO MERIEUX, Societe anonyme
FEATURES  Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /db_xref="taxon:32630"
BASE COUNT   5 a      7 c      4 g      2 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACAGAGGCCA 13
Db      4 GACAGAGGCCA 14

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Job time : 351.346 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 199.363 Seconds
(without alignments)
338.880 Million cell updates/sec

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Perfect score: 30
Sequence: 1 CTGACAGAGCCCACTTCGCGGTGGCAG 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	19	AAV41172 RNA component of h
2	20	66.7	20	19	AAV41173 RNA component of h
3	20	66.7	20	19	AAV41174 RNA component of h
C 4	14	46.7	26	20	AAV71131 PCR primer hTR S32
C 5	14	46.7	30	21	AAAG1649 Mouse Elf-1 revers
6	13	43.3	46	19	AAV24750 Human Type II IL-1
7	12	40.0	20	24	ABL43397 Human chromosome 1
8	12	40.0	21	20	AAZ23852 Rye microsatellit
9	12	40.0	21	20	AAZ36927 S. cereale micros

10	12	40.0	24	20	AAZ36173	PCR primer used to
11	12	40.0	26	22	AAF80328	PCR primer for cDN
C 12	12	40.0	43	22	AAI74547	Human silent SNP c
C 13	12	40.0	46	22	AAI74549	Human silent SNP c
14	12	40.0	50	21	AAA40237	Construct pC2-m9H5
15	11	36.7	12	23	AB141062	Oligonucleotide pr
C 16	11	36.7	13	20	AAK00290	Target DNA sequenc
C 17	11	36.7	13	23	ABF03254	Oligonucleotide SE
18	11	36.7	13	23	ABF03255	Oligonucleotide SE
C 19	11	36.7	13	23	ABH33140	Oligonucleotide SE
20	11	36.7	13	23	ABH33141	Oligonucleotide SE
21	11	36.7	15	16	AAZ52289	Mouse ICAM hammerh
22	11	36.7	18	13	AAQ20414	Detection probe #2
23	11	36.7	18	14	AAQ36192	Detection probe to
24	11	36.7	20	10	AAZ97152	HPV-16 primer (694
25	11	36.7	20	10	AAZ94234	Sequence of probe
C 26	11	36.7	20	11	AAQ06516	Probe/primer TB-5
C 27	11	36.7	20	13	AAQ22888	HCV-Hc59 primer #6
28	11	36.7	20	17	AAZ36613	5' primer for huma
29	11	36.7	20	22	AAQ05954	Human diacylglycer
C 30	11	36.7	20	24	ABL43707	Human chromosome 1
C 31	11	36.7	21	15	AAQ62049	Hen egg white lyso
C 32	11	36.7	21	19	AAV52648	Hepatocyte nuclear
C 33	11	36.7	21	21	AAZ77184	Human biallelic ma
C 34	11	36.7	21	22	AAH01363	aac(3')-Iib resist
C 35	11	36.7	21	22	AAF95841	Human gene single
C 36	11	36.7	21	24	ABA91189	Collectin PCR prim
C 37	11	36.7	22	21	AAC68689	Mouse R35 specific
C 38	11	36.7	22	22	AH01361	aac(3')-Iib resist
39	11	36.7	22	24	ABK86775	PCR primer, 2815,
C 40	11	36.7	23	21	AAQ09876	Human papillomavir
C 41	11	36.7	24	10	AAZ97159	HPV probe. Synthe
C 42	11	36.7	24	10	AAZ94236	Sequence of probe
C 43	11	36.7	24	22	AAF64166	Primer #106. Homo
C 44	11	36.7	24	24	ABQ02087	Oligonucleotide ad
45	11	36.7	24	24	ABQ02284	Oligonucleotide ad

ALIGNMENTS

RESULT 1
AAV41172
ID AAV41172 standard; DNA; 30 BP.
AC AAV41172;
XX AAV41172;
XX 08-OCT-1998 (first entry)
DT RNA component of human telomerase (hTR) antisense oligo 16.
XX RNA component; human telomerase; antisense oligonucleotide; infection;
DE neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
DE KW contraction; sterilisation; immunosuppression; therapeutic; hTR;
DE KW immune system down-regulation; anti-inflammatory therapy; ss.
OS Synthetic.
OS Homo sapiens.
XX
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX 20-DEC-1996; 96US-0770564.
PA (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
DR

```

XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ
Query Match 100.0%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
Db 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
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AAV41173
ID AAV41173 standard; DNA; 20 BP.
XX
XX AAV41173;
XX
XX 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 16ab.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; hTR;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
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XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
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CC polymerase activity of telomerase. These antisense oligonucleotides can
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CC cells in vivo. They can be used in therapeutics for treating or
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CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 30 BP; 6 A; 10 C; 9 G; 5 T; 0 other;
SQ
Query Match 100.0%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
Db 1 CTGACAGAGCCCAACTCTTCGCGTGGCAG 30
RESULT 3
AAV41174
ID AAV41174 standard; DNA; 20 BP.
XX
XX AAV41174;
XX
XX 08-OCT-1998 (first entry)
XX
XX RNA component of human telomerase (hTR) antisense oligo 16bc.
XX
XX RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; hTR;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX WO9828442-A1.
XX
XX 02-JUL-1998.
XX
XX 19-DEC-1997; 97WO-US23619.
XX
XX 20-DEC-1996; 96US-0770565.
XX
XX 20-DEC-1996; 96US-0770564.
XX
XX (GERO-) GERON CORP.
XX
XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
XX
XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
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CC and providing prognosis for a cancer patient. The inhibitory
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CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
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CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
SQ
Query Match 66.7%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

```

PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX Claim 11; Page 65; 80pp; English.
 XX Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridize to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridize to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting the
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;

Query Match 66.7%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCAACTCTTCGGGTGGCAG 30
 Db 1 CCAACTCTTCGGGTGGCAG 20
 |||||

RESULT 4
 ID AAX77131/c
 XX AAX77131 standard; DNA; 26 BP.
 AC AAX77131;
 XX
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE PCR primer hTR S328.
 XX
 XX Cellular senescence; modulator; G66 gene; senescent gene expression;
 KW pGC6; human; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO9925878-A2.
 FN
 XX
 PD 27-MAY-1999.
 XX
 XX 19-NOV-1998; 98WO-US24996.
 PF
 XX 19-NOV-1997; 97US-0974180.
 PR
 XX (GERO-) GERON CORP.
 PA
 XX Funk W;
 PI
 XX WPI; 1999-347496/29.
 DR
 XX New human G66 gene, useful for identifying agents for treating
 XX diseases and/or conditions associated with cell senescence
 PT
 PT
 PS Example 5; Page 74; 79pp; English.
 XX
 XX The invention relates to methods for modulating and identifying cellular

CC senescence. Recombinant expression vectors comprising a recombinant
 CC polynucleotide corresponding to a polynucleotide in a human G66 gene, are
 CC useful for altering senescent gene expression. The vectors and host cells
 CC comprising the vectors are useful for identifying agents that prevent or
 CC modulate senescent gene expression. The polynucleotides are useful for
 CC producing the protein, pGC6 and nucleic acid derivatives. The proteins
 CC encoded are useful for raising antibodies specific for pGC6, which are
 CC useful for isolating pGC6, and for detecting cells comprising pGC6 in
 CC complex cell mixtures. The characterization of the polynucleotides enable
 CC the identification of therapeutic agents that identify and distinguish
 CC between young and senescent cells. This enables treatment of aging
 CC diseases induced or exacerbated by cellular senescence.
 XX

SQ Sequence 26 BP; 1 A; 8 C; 9 G; 8 T; 0 other;

Query Match 46.7%; Score 14; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTGACAGAGCCCAA 14
 Db 14 CTGACAGAGCCCAA 1
 |||||

RESULT 5
 ID AAA61649/c
 XX AAA61649 standard; DNA; 30 BP.
 AC AAA61649;
 XX
 DT 23-OCT-2000 (first entry)
 XX
 DE Mouse Elf-1 reverse PCR primer.
 XX
 KW Elf-1; mouse; transcriptional regulatory factor; rat;
 KW polymorphic variant; immunological disease; allergic disease;
 KW PCR primer; ss.
 XX
 OS Mus sp.
 XX
 XX JP2000135088-A.
 PN
 XX 16-MAY-2000.
 PD
 XX 30-OCT-1998; 98JP-0309595.
 PF
 XX 30-OCT-1998; 98JP-0309595.
 PR
 XX (ASAK) ASAKI BREWERIES LTD.
 PA
 XX WPI; 2000-425802/37.
 DR
 XX A transcription regulating factor Elf-1 cDNA and its polymorphism -
 PT Example 1; Page 4; 21pp; Japanese.

XX The invention relates to three polymorphic variants of a rat
 CC transcriptional regulatory factor Elf-1 (AA803190-B03192) and nucleic
 CC acids encoding them (AAA61645-A61647). The invention also encompasses
 CC the use of Elf-1 for regulating the transcription of a gene in an
 CC expression vector. The cDNA encoding rat Elf-1 variant #1 (AAA61645)
 CC was isolated using PCR primers (AAA61648-A61649) based on mouse Elf-1
 CC cDNA, and the rat Elf-1 variant #2 and #3 cDNAs (AAA61646-A61647) were
 CC subsequently isolated. The Elf-1 cDNA and protein sequences are
 CC potentially useful for the prevention and treatment of immunological and
 CC allergic diseases mediated by Elf-1. Sequences AAA61648-A61649 represent
 CC mouse Elf-1 PCR primers used in an exemplification of the invention to
 CC isolate rat Elf-1 variant #1 cDNA.
 XX

SQ Sequence 30 BP; 9 A; 4 C; 7 G; 10 T; 0 other;

Query Match 46.7%; Score 14; DB 21; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCCCACTCTT 19
DB 19 AGAGCCCACTCTT 6

RESULT 6
AAV34750
ID AAV34750 standard; DNA; 46 BP.
XX
AC AAV34750;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human Type II IL-1R primer #3.
XX

KW Type II interleukin-1 receptor; IL-1R; immune response; inflammation;
KW regulation; soluble; cell surface receptor; treatment; alloantigen;
KW tissue; organ; rejection; transplant; graft-versus-host disease; human;
KW autoimmune dysfunction; T-cell activation; self antigen; primer;
KW rheumatoid arthritis; diabetes mellitus; multiple sclerosis; ss.
XX

OS Synthetic.

OS Homo sapiens.

XX
PN US5767064-A.
XX

XX 16-JUN-1998.

XX 16-MAY-1995; 95US-0442043.

XX 16-MAY-1991; 91US-0701415.

XX 05-JUN-1990; 90US-0534193.

XX 24-AUG-1990; 90US-0573576.

XX 13-DEC-1990; 90US-0627071.

XX 12-JUL-1993; 93US-0091519.

XX 13-MAY-1994; 94US-0242211.

XX 16-MAY-1995; 95US-0442043.

XX (IMV) IMMUNEX CORP.

XX Cosman DJ, Dower SK, Lupton SD, Mosley BA, Sims JE;

XX WPI; 1998-361746/31.

XX Regulation of interleukin-1 mediated immune or inflammatory response

XX in mammal - comprises administering soluble IL-1 receptor protein,

XX used in treatment of e.g. graft versus host disease and multiple

XX sclerosis

XX Example 1; Column 19; 33pp; English.

XX AAV34748-V34756 are primers used in the isolation of human and mouse

XX type II interleukin-1 receptor (IL-1R) which is used in a method to

XX investigate the regulation of the immune or inflammatory response in a

XX mammal. This method involves administering a soluble type-II IL-1

XX receptor protein in an amount effective to bind to IL-1 and prevent its

XX binding to cell-surface IL-1 receptors. The process can be used for

XX treating alloantigen-induced rejection of transplanted tissues or

XX organs, graft-versus-host disease and autoimmune dysfunction dependent

XX upon the activation of T cells against self antigens, selected from

XX rheumatoid arthritis, diabetes mellitus or multiple sclerosis.

XX Sequence 46 BP; 6 A; 12 C; 14 G; 14 T; 0 other;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

RESULT 7

ABL43397

ID ABL43397 standard; DNA; 20 BP.

XX

AC ABL43397;

XX

DT 11-APR-2002 (first entry)

XX

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:441.

XX

KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;

XX genome; PCR primer; ss.

XX Homo sapiens.

XX

PN JP2001321190-A.

XX

PD 20-NOV-2001.

XX

PF 12-MAR-2001; 2001JP-0068285.

XX

PR 10-MAR-2000; 2000JP-0066716.

XX

XX (RIKA) RIKAGAKU KENKYUSHO.

PA (GENO-) GENOTEX YG.

XX

XX WPI; 2002-144136/19.

XX

PT Arraying genome clones -

XX

XX Claim 4; Page 13; 528pp; Japanese.

XX

XX

XX

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XX

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DT 21-JAN-2000 (first entry)
DE .
XX Rye microsatellite marker 13 PCR primer 2.
XX
KW Microsatellite marker; rye; hypervariable genomic region; Poeae;
KW Triticeae; breeding program; DNA fingerprinting; variety; detection;
KW self pollination; cross pollination; cytoplasmic line; genetic mapping;
KW polymorphism; PCR primer; ss.
XX
OS Synthetic.
OS Secale cereale.
XX
XX DE19811506-A1.
XX
PD 21-OCT-1999.
XX
PF 17-MAR-1998; 98DE-1011506.
XX
PR 17-MAR-1998; 98DE-1011506.
XX
PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
DR WPI; 1999-591715/51.
XX
PT New microsatellite markers for rye and closely related grasses, used
PT for genetic analysis and in breeding
XX
PS Claim 6; Page 27; 28pp; German.
XX
CC This invention describes novel microsatellite markers (MSM), based on
CC the hypervariable genomic regions of rye (Secale cereale) and of plants
CC from the tribes Triticeae and Poeae. MSM, which are new genetic markers
CC for rye and closely related species, are used for genetic analysis and
CC in breeding programs. Typical applications are in DNA fingerprinting;
CC identification of varieties; detection of self and cross pollination;
CC characterization of cytoplasmic lines, and genetic mapping (of mono- or
CC poly-genic traits). MSM show a higher degree of polymorphism than known
CC markers (both within and between different rye varieties and lines); can
CC be detected by polymerase chain reaction, so that even very small
CC samples may be analyzed, and generate many alleles per marker locus.
CC AAZ23827-723886 represent the microsatellite marker PCR primers
CC described in the method of the invention.
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
Query Match 40.0%; Score 12; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCCCAACTCTT 19
Db 1 AGCCCAACTCTT 12

RESULT 9
AA36927
ID AAX36927 standard; DNA; 21 BP.
XX
AC AAX36927;
XX
DT 02-JUL-1999 (first entry)
DE S. cereale microsatellite marker PCR primer 26.
XX
KW Microsatellite; marker; PCR primer; rye; plant; Triticeae; Poeae;
KW simple sequence repeat; SSR; sequence tag site; STS; genetic analysis;
KW DNA fingerprinting; variety identification; self fertilization;
KW detection; cross fertilization; cytological line; gene mapping;
KW monogenic trait; polygenic trait; ss.
XX
OS Synthetic.
OS Secale cereale.
XX

PN DE19835109-A1.
XX
PD 15-APR-1999.
XX
PF 04-AUG-1998; 98DE-1035109.
XX
PR 02-OCT-1997; 97DE-1043671.
XX
PA (GVSE-) GVS GES ERWERB & VERWERTUNG LANDWIRTSCHA.
XX
PI Saal B, Wricke G;
XX
DR WPI; 1999-245522/21.
XX
PT Microsatellite markers derived from the genome of rye, useful for
PT genetic mapping as markers of monogenic or polygenic traits
XX
PS Claim 6; Page 16; 28pp; German.
XX
CC This invention describes Secale cereale microsatellite markers based on
CC hypervariable genomic segments of Secale cereale and plants of the
CC tribes Triticeae and Poeae. The microsatellite markers comprise a simple
CC sequence repeat (SSR) marker as sequence tag site (STS), defined by two
CC specific S. cereale defined primers, of mean length 18-26 bases and
CC flanking the microsatellite sequence (MSS). Such markers are useful for
CC genetic analysis of rye, triticale and other species of the tribes
CC Triticeae and Poeae, e.g. for DNA fingerprinting; identification of
CC varieties; detecting self or cross fertilization; studying similarity
CC and relatedness; characterization of cytological lines, or generally any
CC sort of gene mapping. Particularly, they are useful for genetic mapping
CC and marking of mono- or poly-genic traits, selection and evaluation of
CC varietal purity or checking culture stages (particularly in hybrid
CC culture methods), purity of propagative materials, success of
CC self-fertilization and required ratio of components in populations and
CC hybrids. AAX36902-X36965 represent PCR primers used in the method of the
CC invention.
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;
Query Match 40.0%; Score 12; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCCCAACTCTT 19
Db 1 AGCCCAACTCTT 12

RESULT 10
AA36173
ID AAX36173 standard; DNA; 24 BP.
XX
AC AAX36173;
XX
DT 15-JUL-1999 (first entry)
DE PCR primer used to amplify a fragment of ICAM-6 nucleic acid.
XX
KW Intercellular adhesion molecule 6; ICAM-6; drug screening; therapy;
KW intercellular adhesion; inflammatory process; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9920762-A1.
XX
PD 29-APR-1999.
XX
PF 22-OCT-1998; 98WO-US22442.
XX
PR 22-OCT-1997; 97US-0955661.
XX
XX (ICOS-) ICOS CORP.

```

PI Loughney K, Staunton DE, Vazeau R;
 XX WPI; 1999-288308/24.
 XX
 XX New isolated intercellular adhesion molecule-6 used for, e.g.
 PT diagnosis of inflammatory processes
 PT
 XX
 PS Example 15; Page 53; 102pp; English.
 XX
 XX The specification describes an intercellular adhesion molecule
 CC (ICAM)-6 polypeptide. The ICAM-6 polypeptides and polynucleotides
 CC can be used for drug screening and developing products for therapy
 CC involving intercellular adhesion, e.g. in inflammatory processes.
 CC The products can also be used for detection, diagnosis and the
 CC production of transgenic animals. PCR primers AAX36170-73 were used
 CC in the course of the invention.
 XX
 SQ Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;
 Query Match 40.0%; Score 12; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TCACAGAGCCCA 13
 Db 1 TCACAGAGCCCA 12
 RESULT 11
 AAF80328
 ID AAF80328 standard; DNA; 26 BP.
 XX
 AC AAF80328;
 DT 29-JUN-2001 (first entry)
 XX
 DE PCR primer for cDNA encoding the G-protein coupled receptor IGS4.
 KW Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia;
 KW nervous system disorder; psychiatric disorder; Parkinson's disease;
 KW episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke;
 KW cardiovascular disease; heart failure; angina pectoris; obesity; emesis;
 KW motility disorder; myocardial infarction; hypertension; dyslipidemia;
 KW gastrointestinal disorder; inflammatory bowel disease; osteoporosis;
 KW inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
 KW gynecological disorder; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200125269-A2.
 XX
 XX 12-APR-2001.
 XX
 XX 25-SEP-2000; 2000WO-EF09584.
 XX
 XX 24-SEP-1999; 99EP-0203140.
 PR 24-SEP-1999; 99NL-1013140.
 PR 28-JUL-2000; 2000EP-0202683.
 PR 31-JUL-2000; 2000US-0222047.
 XX
 XX (SOLV) SOLVAY PHARM BV.
 PA
 XX
 XX Deleersnijder W, Berger C, Loeken C, Nys G, Venema J;
 PI WPI; 2001-273568/28.
 XX
 XX New G-protein coupled receptors and the polynucleotides encoding them,
 PT useful for preventing, ameliorating or correcting nervous system
 PT disorders, cardiovascular diseases, dyslipidemias, inflammations, pain
 PT or cancers
 XX
 XX Example 1a; Page 39; 102pp; English.
 XX

CC PCR primers AAF80328-30 were used to amplify cDNA encoding a
 CC human G-protein coupled receptor designated IGS4. IGS4 exists in two
 CC polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4
 CC polynucleotides are useful for preventing, ameliorating or correcting
 CC dysfunctions or diseases. These diseases include peripheral nervous
 CC system, psychiatric and central nervous system disorders
 CC (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's
 CC disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases
 CC (e.g. heart failure, angina pectoris, myocardial infarction or
 CC hypertension), dyslipidemias, obesity, emesis, gastrointestinal
 CC disorders (e.g. inflammatory bowel disease or motility disorders),
 CC osteoporosis, inflammations, infections (e.g. bacterial, fungal,
 CC protozoan or viral), pain, cancers, immune disorders, allergies,
 CC sepsis or gynecological disorders. Agonists or antagonists of IGS4 are
 CC effective with regard to disorders of the nervous system, including the
 CC central and peripheral nervous systems, disorders of the gastrointestinal
 CC system, cardiovascular system, skeletal muscle, thyroid, lung or
 CC genitourinary system, or immunological disease. The IGS4 polynucleotides
 CC are useful as diagnostic reagents for detecting under-expression,
 CC overexpression or altered expression of IGS4.
 XX
 SQ Sequence 26 BP; 1 A; 7 C; 9 G; 5 T; 4 other;
 Query Match 40.0%; Score 12; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 TCTTCGCGGTGG 27
 Db 5 TCTTCGCGGTGG 16
 RESULT 12
 AAI74547/c
 ID AAI74547 standard; DNA; 43 BP.
 XX
 AC AAI74547;
 XX
 XX 09-NOV-2001 (first entry)
 DT Human silent SNP containing nucleic acid SEQ:1488.
 DE
 XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 XX protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200140521-A2.
 XX
 XX 07-JUN-2001.
 XX
 XX 30-NOV-2000; 2000WO-US32758.
 XX
 XX 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 PI WPI; 2001-356160/37.
 XX
 XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -
 PT
 XX Claim 1; Page 509; 2653pp; English.
 PS
 XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

SQ Sequence 43 BP; 10 A; 14 C; 6 G; 13 T; 0 other;
 Query Match 40.0%; Score 12; DB 22; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
 |||||
 DB 28 GACAGAGCCCAA 17

RESULT 13
 AAI74549/c
 ID AAI74549 standard; DNA; 46 BP.
 XX
 AC AAI74549;
 XX
 DT 09-NOV-2001 (first entry)
 XX Human silent SNP containing nucleic acid SEQ:1490.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX

OS Homo sapiens.
 XX WO200140521-A2.

PN 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US32758.

XX 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shinkete RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

PS Claim 1; Page 509; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.
 CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its

CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

SQ Sequence 46 BP; 10 A; 15 C; 6 G; 15 T; 0 other;
 Query Match 40.0%; Score 12; DB 22; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAA 14
 |||||
 DB 28 GACAGAGCCCAA 17

RESULT 14
 AAA40237
 ID AAA40237 standard; DNA; 50 BP.

XX
 AC AAA40237;

XX 02-NOV-2000 (first entry)

XX Construct pC2-m8#518 primer P-CC(4).

XX Factor VIII; light chain; LRP; gene therapy; antihemophilic; blood;
 KW low density lipoprotein receptor-related protein; coagulation disorder;
 KW thrombotic system; fibrinolytic system; primer; ss.

XX Unidentified.

XX WO200028021-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-AT00272.

XX 10-NOV-1998; 99AT-0001872.

XX (BAXT) BAXTER AG.

XX Lenting PJ, Van Mourik JA, Mertens K, Pannekoek H, Turecek P;
 PI Schwarz H, Scheiflinger F;

XX WPI; 2000-376538/32.

XX New modified form of factor VIII, useful for treating hemophilia, has
 PT altered binding to low density lipoprotein-related protein, resulting
 PT in extended in vivo half-life -

XX Example XI; Page 35; 57pp; German.

XX This invention describes a novel factor VIII polypeptide (I) with factor
 CC VIII:C activity which has a modification in at least one of the A3, C1
 CC and/or C2 domains of the light chain that modifies binding affinity to
 CC low density lipoprotein receptor-related protein (LRP). Independent
 CC claims are also included for the following: (1) DNA (II) that encodes
 CC (I); (2) an expression vector containing (II); (3) transformed cells and
 CC their descendants containing (II); (4) recombinant production of (I) by
 CC culturing cells of (C); and (5) pharmaceutical composition containing a
 CC factor VIII molecule (Ia) with factor VIII:C activity plus an LRP
 CC antagonist (III). The products of the invention have antihemophilic
 CC activity. (I) has reduced affinity for LRP, a receptor involved in
 CC clearance of factor VIII from the blood. (I), optionally formulated with
 CC an antagonist of LRP, is used for treatment of coagulation disorders,
 CC specifically hemophilia A. It may also be used to treat subjects with
 CC disorders of the thrombotic or fibrinolytic systems, e.g. before,
 CC during or after surgery. Nucleic acid that encodes (I) can be used

CC similarly in gene therapy. The light chain modifications reduce clearance
CC of factor VIII protein from the blood, resulting in longer in vivo
CC half-life (particularly at least 90% greater than wild type) and
CC increased stability, in vivo or in vitro. The modifications do not
CC adversely affect procoagulant activity. This sequence represents a primer
CC used in the construction of the plasmid pC2-m9#518 which contains the
CC Factor VIII light chain C2 region which is described in the method of the
CC invention.

XX Sequence 50 BP; 11 A; 16 C; 15 G; 8 T; 0 other;

Query Match 40.0%; Score 12; DB 21; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCCCACTCT 18

|||||

Db 31 GAGCCCACTCT 42

RESULT 15

ABI41062

ID ABI41062 standard; DNA; 12 BP.

XX AC ABI41062;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 341035 for detecting SNP TSC0010735.

XX SNP; single-nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW Central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.

OS

FN WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX Claim 1; SEQ ID 341035; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABI00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 other;

Query Match 36.7%; Score 11; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 5.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CAACCTCTTCGC 22

|||||

Db 2 CAACCTCTTCGC 12

Search completed: June 23, 2003, 05:43:36

Job time : 201.67 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 241.076 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-5

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Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	43.3	46	9 US-10-199-209-5	Sequence 5, Appl
2	12	40.0	25	9 US-10-098-263B-31566	Sequence 31566, A
3	12	40.0	25	9 US-10-098-263B-110352	Sequence 110352,
4	12	40.0	31	9 US-09-288-971-6	Sequence 6, Appl
5	12	40.0	31	9 US-09-288-971-10	Sequence 10, Appl
6	11	36.7	18	10 US-09-969-373-3187	Sequence 3187, Ap
7	11	36.7	21	9 US-10-222-334-65	Sequence 65, Appl
8	11	36.7	24	9 US-09-940-185-2094	Sequence 2094, Ap
9	11	36.7	24	9 US-09-940-185-2291	Sequence 2291, Ap
10	11	36.7	24	10 US-09-898-779-110	Sequence 110, App
11	11	36.7	25	9 US-09-592-665-205	Sequence 205, App
12	11	36.7	25	9 US-10-098-263B-97446	Sequence 97446, A
13	11	36.7	25	9 US-10-098-263B-129624	Sequence 129624,
14	11	36.7	26	10 US-09-118-276-16	Sequence 16, Appl
15	11	36.7	36	8 US-08-961-888-12	Sequence 12, Appl
16	11	36.7	36	9 US-09-824-017-24	Sequence 24, Appl
17	11	36.7	36	9 US-09-386-118A-24	Sequence 24, Appl
18	11	36.7	36	9 US-10-002-050-29	Sequence 29, Appl
19	11	36.7	36	9 US-10-002-304-29	Sequence 29, Appl

20	11	36.7	36	12	US-10-003-152-29	Sequence 29, Appl
21	11	36.7	38	9	US-09-824-017-25	Sequence 25, Appl
22	11	36.7	38	9	US-09-986-118A-25	Sequence 25, Appl
23	10	33.3	17	9	US-09-818-875-1383	Sequence 1383, Ap
24	10	33.3	17	9	US-09-818-875-1384	Sequence 1384, Ap
25	10	33.3	17	9	US-09-818-875-1387	Sequence 1387, Ap
26	10	33.3	17	9	US-09-818-875-1388	Sequence 1388, Ap
27	10	33.3	19	9	US-10-093-958-22	Sequence 22, Appl
28	10	33.3	19	9	US-10-291-022-2	Sequence 2, Appl
29	10	33.3	20	9	US-09-971-894-12	Sequence 12, Appl
30	10	33.3	20	9	US-10-090-011-45	Sequence 45, Appl
31	10	33.3	20	9	US-09-915-814-161	Sequence 161, Appl
32	10	33.3	20	10	US-09-909-849-17	Sequence 17, Appl
33	10	33.3	20	10	US-09-263-959-1126	Sequence 1126, Ap
34	10	33.3	21	9	US-09-853-925-420	Sequence 420, App
35	10	33.3	21	9	US-10-082-804-3	Sequence 3, Appl
36	10	33.3	21	9	US-09-909-567B-23	Sequence 23, Appl
37	10	33.3	21	9	US-10-085-906-387	Sequence 387, App
38	10	33.3	21	10	US-09-901-484A-420	Sequence 420, App
39	10	33.3	22	9	US-09-487-318-11	Sequence 11, Appl
40	10	33.3	22	10	US-09-930-251-16	Sequence 16, Appl
41	10	33.3	22	10	US-09-930-251-17	Sequence 17, Appl
42	10	33.3	22	10	US-09-930-251-18	Sequence 18, Appl
43	10	33.3	23	9	US-10-090-887-8	Sequence 8, Appl
44	10	33.3	23	10	US-09-808-382-4	Sequence 4, Appl
45	10	33.3	24	9	US-09-940-185-2918	Sequence 2918, Ap

ALIGNMENTS

RESULT 1
US-10-199-209-5
; Sequence 5, Application US/10199209
; Publication No. US20030060616A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; Cosman, David J.
; Lupton, Stephen D.
; Mosley, Bruce A.
; Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5
Query Match 43.3%; Score 13; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AACTCTTCGCGGT 25
|||||
DB 25 AACTCTTCGCGGT 37

RESULT 2
US-10-098-263B-31566
; Sequence 31566, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-31566
Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCTTCGCGGTGG 27
|||||
DB 5 TCTTCGCGGTGG 16

RESULT 3
US-10-098-263B-110352
; Sequence 110352, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110352
Query Match 40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCG 21
|||||
DB 3 CCCAACTCTTCG 14

RESULT 4
US-09-288-971-6/c
; Sequence 6, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288,971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-6
Query Match 40.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
|||||
DB 28 CTGACAGAGCCC 17

RESULT 5
US-09-288-971-10
; Sequence 10, Application US/09288971
; Publication No. US20030036055A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: METHODS AND KITS TO ENRICH FOR DESIRED NUCLEIC ACID
; FILE REFERENCE: 04121.0117
; CURRENT APPLICATION NUMBER: US/09/288,971
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-288-971-10
Query Match 40.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCC 12
|||||
DB 4 CTGACAGAGCCC 15

RESULT 6
US-09-969-373-3187
; Sequence 3187, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:

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; APPLICANT: Effertz, Roger J.
; APPLICANT: Haughe, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 08/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3187
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3187

Query Match 36.7%; Score 11; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCCAACTCTT 19
Db 7 GCCCAACTCTT 17

RESULT 7

US-10-222-334-65/c
; Sequence 65, Application US/10222334
; Publication No. US20030073116A1
; GENERAL INFORMATION:
; APPLICANT: Gineburg, David
; APPLICANT: Levy, Gallia
; APPLICANT: Tsai, Han-Mou
; TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
; FILE REFERENCE: UM-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/312,834
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 65
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-222-334-65

Query Match 36.7%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCC 11
Db 11 CTGACAGAGCC 1

RESULT 8

US-09-940-185-2094/c
; Sequence 2094, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948

; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2094
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2094

Query Match 36.7%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCACTCTTCGC 22
Db 11 CCACTCTTCGC 1

RESULT 9

US-09-940-185-2291
; Sequence 2291, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2291
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2291

Query Match 36.7%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCC 12
Db 7 TGACAGAGCCC 17

RESULT 10

US-09-898-779-110/c
; Sequence 110, Application US/09898779
; Patent No. US20020106657A1
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Maren T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; FILE REFERENCE: 18810-82302
; CURRENT APPLICATION NUMBER: US/09/898,779
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/347,114
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 110

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-779-110

Query Match      36.7%; Score 11; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGACAGAGCC 11
        |||||
Db      19 CTGACAGAGCC 9

RESULT 11
US-09-992-665-205
; Sequence 205, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kata Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-205

Query Match      36.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACAGAGCCCA 13
        |||||
Db      3 GACAGAGCCCA 13

RESULT 12
US-10-098-263B-97446
; Sequence 97446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 97446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-97446

Query Match      36.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTCCTCGCGGT 25
        |||||
Db      3 CTCCTCGCGGT 13

RESULT 13
US-10-098-263B-129624
; Sequence 129624, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-129624

Query Match      36.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCAACTCTTCG 21
        |||||
Db      9 CCAACTCTTCG 19

RESULT 14
US-09-118-276-16
; Sequence 16, Application US/09118276
; Patent No. US20010011381A1
; GENERAL INFORMATION:
; APPLICANT: BABYCHUK, ELENA;
; APPLICANT: KUSHNIR, SERGEI;
; APPLICANT: DE BLOCK, MARC;
; APPLICANT: INZE, DIRK
; TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SIXBEY, FRIEDMAN, LEEDOM, & FERGUSON
; STREET: 8180 GREENSBORO DRIVE, SUITE 800
; CITY: MCLEAN,
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2" DISKETTE
; COMPUTER: IBM-COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/118,276
; FILING DATE: 17-JUL-1998
; PRIOR APPLICATION DATA: NONE
; ATTORNEY/AGENT INFORMATION:
; NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH H.
; REGISTRATION NUMBER: 31,196; 43,077
; REFERENCE/DOCKET NUMBER: 6201-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 790-9110
; TELEFAX: (703) 883-0370
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 BASES
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
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TOPOLOGY: LINEAR
US-09-118-276-16

Query Match 36.7%; Score 11; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCCAACTCTTC 20
DB 11 CCCAACTCTTC 21

RESULT 15

US-08-961-888-12
; Sequence 12, Application US/08961888
; Patent No. US20010016351A1
; GENERAL INFORMATION:
; APPLICANT: Padgett, Kerstien
; APPLICANT: Sorge, Joseph
; TITLE OF INVENTION: No. US20010016351A1 Vector For Gene Expression
; TITLE OF INVENTION: In Prokaryotic And Eukaryotic Systems
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,888
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-7451
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-961-888-12

Query Match 36.7%; Score 11; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCTTCGCGGT 25
DB 11 CTCTTCGCGGT 21

Search completed: June 23, 2003, 20:01:30
Job time : 242.076 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 46.9721 Seconds
(without alignments)
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Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTTTCGGGTGGCAG 30

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Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	66.7	20	2	US-08-770-565-6
3	20	66.7	20	2	US-08-770-565-7
4	14	46.7	26	3	US-08-974-180-33
5	14	46.7	45	6	5198342-4
6	13	43.3	46	1	US-08-091-519-5
7	13	43.3	46	1	US-08-106-507-7
8	13	43.3	46	1	US-08-442-043A-5
9	13	43.3	46	5	PCT-US91-03478-5
10	11	36.7	15	2	US-08-292-620A-451
11	11	36.7	15	3	US-09-071-845-451
12	11	36.7	18	1	US-08-273-776-12
13	11	36.7	18	1	US-08-255-892-42
14	11	36.7	20	1	US-08-358-995-2
15	11	36.7	20	2	US-08-473-020A-13
16	11	36.7	20	3	US-08-913-547-3
17	11	36.7	21	4	US-08-927-219-29
18	11	36.7	24	1	US-09-347-114A-110
19	11	36.7	30	4	US-08-495-743-60
20	11	36.7	30	1	US-08-495-739-60
21	11	36.7	30	1	US-08-495-741-60
22	11	36.7	30	4	US-08-062-023-60
23	11	36.7	36	4	US-08-944-368A-24
24	11	36.7	36	4	US-09-820-764-24
25	11	36.7	38	1	US-08-664-449-61
26	11	36.7	38	4	US-08-944-368A-25
27	11	36.7	38	4	US-09-820-764-25

c 28	11	36.7	42	4	US-09-051-363-23	Sequence 23, Appli
c 29	10	33.3	11	1	US-07-778-233B-3	Sequence 3, Appli
c 30	10	33.3	11	1	US-07-963-321-3	Sequence 3, Appli
c 31	10	33.3	11	1	US-08-290-641-3	Sequence 3, Appli
c 32	10	33.3	11	1	US-08-548-540-3	Sequence 3, Appli
c 33	10	33.3	11	5	PCT-US96-09809-3	Sequence 3, Appli
c 34	10	33.3	17	2	US-08-292-620A-1733	Sequence 1733, Ap
c 35	10	33.3	17	3	US-09-071-845-1733	Sequence 1733, Ap
c 36	10	33.3	17	4	US-08-584-040-5345	Sequence 5345, Ap
c 37	10	33.3	18	1	US-08-539-252-1	Sequence 1, Appli
c 38	10	33.3	18	1	US-08-436-074-1	Sequence 1, Appli
c 39	10	33.3	18	4	US-09-050-159-5	Sequence 5, Appli
c 40	10	33.3	18	5	PCT-US96-06352-1	Sequence 1, Appli
c 41	10	33.3	18	5	PCT-US96-06583-1	Sequence 1, Appli
c 42	10	33.3	20	2	US-08-578-551-10	Sequence 10, Appli
c 43	10	33.3	20	2	US-08-473-020A-14	Sequence 14, Appli
c 44	10	33.3	20	2	US-09-289-368-52	Sequence 52, Appli
c 45	10	33.3	20	2	US-09-190-982-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-5

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.5e-09;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTTTCGGGTGGCAG 30

Db 1 CTGACAGAGCCCACTTCGCGGTGGCAG 30

RESULT 2
US-08-770-565-6
; Sequence 6, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCACTTC 20
Db 1 CTGACAGAGCCCACTTC 20

RESULT 3
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-7

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCAACTCTTCGCGGTGGCAG 30
Db 1 CCAACTCTTCGCGGTGGCAG 20

RESULT 4
US-08-974-180-33/c
; Sequence 33, Application US/08974180
; Patent No. 6025194
; GENERAL INFORMATION:
; APPLICANT: Funk, Walter
; TITLE OF INVENTION: Methods for Modulating and Identifying
; TITLE OF INVENTION: Cellular Senescence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Geron Corporation
; STREET: 230 Constitution Drive
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,180
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaster, Kevin R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 473-7779
; TELEFAX: (650) 473-8654
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:


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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..26
; OTHER INFORMATION: /note= "primer hTR S328"
US-08-974-180-33

Query Match 46.7%; Score 14; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGACAGAGCCCA 14
Db 14 CTGACAGAGCCCA 1

RESULT 5
5198342-4
; Patent No. 5198342
; APPLICANT: MALIISZEWSKI; CHARLES R.
; TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/548,059
; FILING DATE: 05-JUL-1990
; SEQ ID NO: 4
; LENGTH: 45
5198342-4

Query Match 46.7%; Score 14; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 CAACTCTTCGCGGT 25
Db 23 CAACTCTTCGCGGT 36

RESULT 6
US-08-091-519-5
; Sequence 5, Application US/08091519
; Patent No. 5350683
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/701,415
; FILING DATE:

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; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-091-519-5

Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 AACTCTTCGCGGT 25
Db 25 AACTCTTCGCGGT 37

RESULT 7
US-08-106-507-7
; Sequence 7, Application US/08106507
; Patent No. 5573924
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: GOODWIN, RAYMOND G.
; APPLICANT: GIRI, JUDITH G.
; APPLICANT: ARMITAGE, RICHARD J.
; TITLE OF INVENTION: CD27 LIGAND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,507
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,648
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WIGHT, CHRISTOPHER L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2809-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: oligonucleotide
US-08-106-507-7

Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AACTCTTCGCGGT 25
|||||
Db 25 AACTCTTCGCGGT 37

RESULT 8

US-08-442-043A-5
; Sequence 5, Application US/08442043A
; Patent No. 5767064

GENERAL INFORMATION:

; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.

; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,043A
; FILING DATE: 16-MAY-1995

CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,192
; FILING DATE: 05-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,415
; FILING DATE: 16-MAY-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,519
; FILING DATE: 12-JULY-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,211
; FILING DATE: 13-MAY-1994

ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2003-F
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-442-043A-5

Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AACTCTTCGCGGT 25
|||||
Db 25 AACTCTTCGCGGT 37

RESULT 9

PCT-US91-03478-5

; Sequence 5, Application PC/TUS9103478
; GENERAL INFORMATION:

; APPLICANT: Sims, John E.
; APPLICANT: Cosman, David J.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Dower, Steven K.

; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03478
; FILING DATE: 19910517

CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990

ATTORNEY/AGENT INFORMATION:

; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644

INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
PCT-US91-03478-5

Query Match 43.3%; Score 13; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AACTCTTCGGGT 25
Db 25 AACTCTTCGGGT 37
|||||

RESULT 10
US-08-292-620A-451
; Sequence 451, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 451:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 36.7%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 8.1e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCAACTCTTC 20
|||||

Db 1 CCCAACUCUC 11
|||||

RESULT 11
US-09-071-845-451
; Sequence 451, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 451:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 36.7%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 8.1e+02;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CCCAACTCTTC 20
|||||

Db 1 CCCAACUCUC 11
|||||

RESULT 12
US-08-273-776-12
; Sequence 12, Application US/08273776
; Patent No. 5510084

```

; GENERAL INFORMATION:
; APPLICANT: Cros, Philippe
; APPLICANT: Allibert, Patrice Andre
; APPLICANT: Dalbon, Pascal Thierry
; TITLE OF INVENTION: Process for immobilizing a Nucleic Acid
; TITLE OF INVENTION: Fragment by Passive Attachment to a Solid Substrate, the
; TITLE OF INVENTION: Solid Substrate thus Obtained and Its Use.
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff and Berridge
; STREET: 700 S. Washington St.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,776
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/913,953
; FILING DATE: 17-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB28083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-273-776-12

Query Match 36.7%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
DB 4 GACAGAGCCCA 14

RESULT 13
US-08-255-892-42
; Sequence 42, Application US/08255892
; Patent No. 5695926
; GENERAL INFORMATION:
; APPLICANT: CROS, PHILIPPE
; APPLICANT: ALLIBERT, PATRICE
; APPLICANT: MALLET, FRANCOIS
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON

; GENERAL INFORMATION:
; APPLICANT: Cros, Philippe
; APPLICANT: Allibert, Patrice Andre
; APPLICANT: Dalbon, Pascal Thierry
; TITLE OF INVENTION: Process for immobilizing a Nucleic Acid
; TITLE OF INVENTION: Fragment by Passive Attachment to a Solid Substrate, the
; TITLE OF INVENTION: Solid Substrate thus Obtained and Its Use.
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff and Berridge
; STREET: 700 S. Washington St.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,776
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/913,953
; FILING DATE: 17-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB28083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-273-776-12

Query Match 36.7%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
DB 4 GACAGAGCCCA 14

RESULT 14
US-08-358-995-2/c
; Sequence 2, Application US/08358995
; Patent No. 5741638
; GENERAL INFORMATION:
; APPLICANT: AKIO YAMANE
; TITLE OF INVENTION: Microtiter Well For Detecting
; TITLE OF INVENTION: Nucleic Acid
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,995
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,572
; FILING DATE: January 14, 1993
; APPLICATION NUMBER: 07/722,673
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.

```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,892
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/834,543
; FILING DATE: 11-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DEEVER, DONALD B.
; REGISTRATION NUMBER: 23,048
; REFERENCE/DOCKET NUMBER: 1032/94109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-255-892-42

Query Match 36.7%; Score 11; DB 1; Length 18;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 GACAGAGCCCA 14

RESULT 14
US-08-358-995-2/c
; Sequence 2, Application US/08358995
; Patent No. 5741638
; GENERAL INFORMATION:
; APPLICANT: AKIO YAMANE
; TITLE OF INVENTION: Microtiter Well For Detecting
; TITLE OF INVENTION: Nucleic Acid
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,995
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,572
; FILING DATE: January 14, 1993
; APPLICATION NUMBER: 07/722,673
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.

```

REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "having biotin at
OTHER INFORMATION: 5' end with a spacer"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-358-995-2

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Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 GACAGAGCCCA 8

RESULT 15

US-08-473-020A-13/c
Sequence 13, Application US/08473020A
Patent No. 5877273
GENERAL INFORMATION:

APPLICANT: Hance, Allan J
APPLICANT: Grandchamp-Desraux, Bernard
APPLICANT: Levy-Frebault, Veronique
APPLICANT: Gicquel, Brigitte
TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
applications to the synthesis or detection of nucleic

TITLE OF INVENTION: acids, products of expression of such sequences and
application as immunogenic compositions.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,020A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-473-020A-13

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Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 CGCGGTGGCAG 1

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Job time : 48.9721 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 2516.18 Seconds
(without alignments)
299.770 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
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 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
 ; TITLE OF INVENTION: RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/23619
 ; FILING DATE: Not yet assigned
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,564
 ; FILING DATE: 20-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,565
 ; FILING DATE: 20-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 15389-27PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; NAME/KEY:
 ; LOCATION: 1..30
 ; OTHER INFORMATION: /note="oligo 16"
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 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30
 RESULT 2
 US-08-770-564A-5
 ; Sequence 5, Application US/08770564A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ron
 ; APPLICANT: Weinrich, Scott L.
 ; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
 ; TITLE OF INVENTION: Against the RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,564A
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
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 US-08-770-564A-5
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 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 RESULT 3
 US-08-521-634-15/c

Sequence 15, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-15

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Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 24 GACAGAGCCCAACTCTTCGGGTG 1
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Sequence 6, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 16ab"
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Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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APPLICANT:
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APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 16bc"
PCT-US97-23619-7

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCGGGTGGCAG 30
Db 1 CCAACTCTTCGGGTGGCAG 20

RESULT 6
US-08-770-564A-6
; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-002200US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-6

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20

RESULT 7
US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-7

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCGGGTGGCAG 30
Db 1 CCAACTCTTCGGGTGGCAG 20

RESULT 8

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US-09-956-604-105231/c
; Sequence 105231, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-105231

Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CAACTCTTCGCGGTGGCA 29
DB      21 CAACTCTTCGCGGTGGCA 4

RESULT 9
US-09-956-604A-105231/c
; Sequence 105231, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604A-105231

Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CAACTCTTCGCGGTGGCA 29
DB      21 CAACTCTTCGCGGTGGCA 4

US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604B-105231

Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CAACTCTTCGCGGTGGCA 29
DB      21 CAACTCTTCGCGGTGGCA 4
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Query Match          60.0%; Score 18; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CAACTCTTCGCGGTGGCA 29
DB      21 CAACTCTTCGCGGTGGCA 4

RESULT 11
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

Query Match          60.0%; Score 18; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CAACTCTTCGCGGTGGCA 29
DB      21 CAACTCTTCGCGGTGGCA 4

RESULT 12
US-09-396-196F-124326
; Sequence 124326, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-124326

Query Match          43.3%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGACAGAGCCCAA 14
DB      2 TGACAGAGCCCAA 14

RESULT 13
US-09-396-196G-124326
```

; Sequence 124326, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 124326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124326

Query Match 43.3%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCA 14
|||
Db 2 TGACAGAGCCCA 14

RESULT 14

US-09-660-220-66821/c
; Sequence 66821, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 66821
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66821

Query Match 43.3%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTC 17
|||
Db 16 CAGAGCCCACTC 4

RESULT 15

US-09-660-220-66822/c
; Sequence 66822, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981

; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 66822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank M95740
US-09-660-220-66822

Query Match 43.3%; Score 13; DB 26; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTC 17
|||
Db 13 CAGAGCCCACTC 1

Search completed: June 23, 2003, 16:08:18
Job time : 2517.25 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 1316.89 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-5

Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTTCGCGGTGGCAG 30

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0 8653682

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	73.3	23	1	PCT-US03-04088-522
C 2	19	63.3	21	1	PCT-US03-04088-540
C 3	19	63.3	21	1	PCT-US03-04088-544
C 4	19	63.3	21	1	PCT-US03-04088-548
C 5	19	63.3	21	1	PCT-US03-04088-552
C 6	19	63.3	21	1	PCT-US03-04088-556
C 7	19	63.3	21	1	PCT-US03-04088-560
C 8	18	60.0	19	1	PCT-US03-04088-23
C 9	18	60.0	21	1	PCT-US03-04088-287
C 10	16	53.3	21	1	PCT-US03-04088-588
C 11	16	53.3	23	1	PCT-US03-04088-530
C 12	14	46.7	21	1	PCT-US03-04088-258
C 13	14	46.7	21	1	PCT-US03-04088-593
C 14	14	46.7	25	12	US-60-427-808-47221
C 15	14	46.7	25	12	US-60-427-808-699316
C 16	14	46.7	25	12	US-60-427-836-401411
C 17	14	46.7	25	12	US-60-427-836-529892
C 18	13	43.3	19	1	PCT-US03-04088-22
C 19	13	43.3	19	1	PCT-US03-04088-286
C 20	13	43.3	20	1	PCT-US02-21361-189

Sequence 189, App	20	9	US-10-188-186-189	43.3	13	21
Sequence 306, App	20	9	US-10-160-619-306	43.3	22	23
Sequence 315, App	20	9	US-10-160-619-315	43.3	23	23
Sequence 66821, A	25	6	US-09-660-222-66821	43.3	C 24	25
Sequence 66822, A	25	6	US-09-660-222-66822	43.3	C 25	25
Sequence 66827, A	25	6	US-09-660-222-66827	43.3	C 26	26
Sequence 66828, A	25	6	US-09-660-222-66828	43.3	C 27	27
Sequence 66829, A	25	6	US-09-660-222-66829	43.3	C 28	28
Sequence 281714, A	25	9	US-10-355-577-281714	43.3	30	30
Sequence 534052, A	25	9	US-10-355-577-534052	43.3	31	31
Sequence 625356, A	25	9	US-10-355-577-625356	43.3	C 32	32
Sequence 2606, App	25	12	US-60-427-808-2606	43.3	C 33	33
Sequence 435724, A	25	12	US-60-427-808-435724	43.3	C 34	34
Sequence 467623, A	25	12	US-60-427-808-467623	43.3	C 35	35
Sequence 503841, A	25	12	US-60-427-808-503841	43.3	C 36	36
Sequence 95568, App	25	12	US-60-427-836-95568	43.3	C 37	37
Sequence 95550, A	25	12	US-60-427-836-95550	43.3	C 38	38
Sequence 198381, A	25	12	US-60-427-836-198381	43.3	C 39	39
Sequence 331174, A	25	12	US-60-427-836-331174	43.3	40	40
Sequence 14041, A	21	10	US-10-199-209A-5	40.0	41	41
Sequence 4756, App	24	9	US-10-293-338-4756	40.0	42	42
Sequence 209, App	25	6	US-09-660-222-209	40.0	43	43
Sequence 6083, App	25	6	US-09-660-222-6083	40.0	C 44	44
Sequence 27816, A	25	6	US-09-660-222-27816	40.0	C 45	45

ALIGNMENTS

RESULT 1

PCT-US03-04088-522/c
; Sequence 522, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 522
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
; OTHER INFORMATION: region
PCT-US03-04088-522

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTCG 22
 Db 22 CTGACAGAGCCCAACTCTTCG 1

RESULT 2
 PCT-US03-04088-540/c
 ; Sequence 540, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT FILING DATE: 2003-04-28
 ; PCT-US03-04088-540
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 540
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-540

Query Match 63.3%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGACAGAGCCCAACTCTTC 20
 Db 19 TGACAGAGCCCAACTCTTC 1

RESULT 3
 PCT-US03-04088-544
 ; Sequence 544, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT FILING DATE: 2003-04-28
 ; PCT-US03-04088-544
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 544
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-544

Query Match 63.3%; Score 19; DB 1; Length 21;
 Best Local Similarity 78.9%; Pred. No. 0.46;
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCACAGAGCCCAACTCTTC 20
 Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 4
 PCT-US03-04088-548/c
 ; Sequence 548, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT FILING DATE: 2003-04-28
 ; PCT-US03-04088-548
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 548
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1)

```
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

```
Query Match 63.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
   |||||
Db 19 TGACAGAGCCCAACTCTTC 1
```

```
RESULT 5
PCT-US03-04088-552
Sequence 552, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 552
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
FEATURE:
OTHER INFORMATION: antisense region
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

```
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
```

```
Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.46;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTC 20
   |||||
Db 1 UGACAGAGCCCAACUCUUC 19
```

```
RESULT 6
PCT-US03-04088-556/c
Sequence 556, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 556
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
FEATURE:
OTHER INFORMATION: region
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(6)
OTHER INFORMATION: 2'-deoxy
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxybasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety
PCT-US03-04088-556
```

```
Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 19 TGACAGAGCCCAACTCTTC 1
```

```
RESULT 7
PCT-US03-04088-560
; Sequence 560, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
```

```
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 560
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(8)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-560

Query Match 63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.46;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGACAGAGCCCAACTCTTC 20
Db 1 UGACAGAGCCCAACUCUUC 19

RESULT 8
PCT-US03-04088-23/c
; Sequence 23, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
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;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 23
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
;; OTHER INFORMATION: region
PCT-US03-04088-23

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCT 18
Db 18 CTGACAGAGCCCAACTCT 1

RESULT 9
PCT-US03-04088-287
;; Sequence 287, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; PRIOR FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 287
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
;; OTHER INFORMATION: region
PCT-US03-04088-287

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.8;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGACAGAGCCCAACTCT 18
Db 2 CUGACAGAGCCCAACUCU 19

RESULT 10
PCT-US03-04088-588/c
;; Sequence 588, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; PRIOR FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 588
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-588

Query Match 53.3%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTCTTCGCGGTGGCAG 30
Db 21 CTCTTCGCGGTGGCAG 6

RESULT 11
PCT-US03-04088-530/c
;; Sequence 530, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; PRIOR FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION-NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 530
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-530

 Query Match 53.3%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 15 CTCTTCGCGGTGGCAG 30
 |||||
 Db 23 CTCTTCGCGGTGGCAG 8

 RESULT 12
 PCT-US03-04088-258/c
 ; Sequence 258, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 258
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
 ; OTHER INFORMATION: region
 PCT-US03-04088-258

Query Match 46.7%; Score 14; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTTCGCGGTGGCAG 30
 |||||
 Db 19 CTTCGCGGTGGCAG 6

 RESULT 13
 PCT-US03-04088-593
 ; Sequence 593, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 593
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
 ; OTHER INFORMATION: antisense region
 PCT-US03-04088-593

 Query Match 46.7%; Score 14; DB 1; Length 21;
 Best Local Similarity 78.6%; Pred. No. 3.7e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTTCGCGGTGGCAG 30
 |||||
 Db 1 CUUCGCGGUGGCAG 14

 RESULT 14
 US-60-427-808-47221
 ; Sequence 47221, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528-
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 47221
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; OTHER INFORMATION: region
 US-60-427-808-47221

 Query Match 46.7%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTT 19
 |||||
 Db 2 AGAGCCCAACTCTT 15

RESULT 15

US-60-427-808-699316
 ; Sequence 699316, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 699316
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-699316

Query Match 46.7%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCTTC 20
 |||||
 Db 3 GAGCCCAACTCTTC 16

Search completed: June 23, 2003, 19:12:11
 Job time : 1317.89 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1546.73 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGACCCCACTTCGCGGTGGCAG 30

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_ges:*
- 18: em_ges_hum:*
- 19: em_ges_inv:*
- 20: em_ges_pln:*
- 21: em_ges_vrt:*
- 22: em_ges_fun:*
- 23: em_ges_nam:*
- 24: em_ges_mus:*
- 25: em_ges_other:*
- 26: em_ges_pro:*
- 27: em_ges_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	40.0	46	17 AZ379320	AZ379320 1M0134P22
C 2	11	36.7	12	13 BM398341	BM398341 5009-0-44
C 3	11	36.7	19	13 BM401213	BM401213 5009-0-84
C 4	11	36.7	20	13 BM395007	BM395007 50072-2-7
C 5	11	36.7	21	17 AZ781467	AZ781467 2M0019F23
C 6	11	36.7	22	17 AZ393281	AZ393281 1M0156H13

7	11	36.7	24	17	AZ309564	AZ309564 1M0016B09
8	11	36.7	26	13	BM399150	BM399150 5009-0-54
9	11	36.7	33	13	BM398611	BM398611 5009-0-47
C 10	11	36.7	34	17	AL759526	AL759526 Arabidops
C 11	11	36.7	37	13	BJ063841	BJ063841
C 12	11	36.7	40	17	BH851915	BH851915 SALK_0737
13	11	36.7	44	13	BM400948	BM400948 5009-0-80
14	11	36.7	45	13	BM397151	BM397151 5009-0-29
C 15	11	36.7	47	10	BES36289	BES36289 601062681
16	11	36.7	49	9	AA813480	AA813480 a167a09.8
17	11	36.7	50	9	AU106839	AU106839 AU106839
18	10	33.3	14	13	BM396493	BM396493 5009-0-21
19	10	33.3	17	13	BM396941	BM396941 5009-0-27
C 20	10	33.3	18	14	BM675715	BM675715 TOH602767
21	10	33.3	20	13	BM400293	BM400293 5009-0-70
22	10	33.3	20	13	BM400757	BM400757 5009-0-78
23	10	33.3	21	13	BM401335	BM401335 5009-0-9-
C 24	10	33.3	22	9	AI687266	AI687266 tp94d10.x
25	10	33.3	23	17	AZ331549	AZ331549 1M0059K02
26	10	33.3	23	17	AZ627985	AZ627985 1M0476006
27	10	33.3	24	13	BM399103	BM399103 5009-0-53
C 28	10	33.3	25	9	AI647975	AI647975 UK38F04.x
29	10	33.3	25	13	BM397307	BM397307 5009-0-30
30	10	33.3	26	13	BM397299	BM397299 5009-0-30
C 31	10	33.3	28	17	AZ939438	AZ939438 2M0198121
32	10	33.3	29	13	BM400082	BM400082 5009-0-66
C 33	10	33.3	29	17	AZ412468	AZ412468 1M0185M20
C 34	10	33.3	30	17	AZ310102	AZ310102 1M0018B24
35	10	33.3	33	13	BM396856	BM396856 5009-0-25
36	10	33.3	37	9	AI572041	AI572041 tr72h02.x
37	10	33.3	37	12	BG423450	BG423450 602449304
C 38	10	33.3	37	13	BI765481	BI765481 603050546
39	10	33.3	38	14	H45829	H45829 Y081b05.81
40	10	33.3	39	17	AZ773780	AZ773780 2M0001802
41	10	33.3	41	13	BM398089	BM398089 5009-0-40
42	10	33.3	42	13	BM400119	BM400119 5009-0-66
C 43	10	33.3	42	17	AZ616105	AZ616105 1M0445G18
44	10	33.3	43	9	AI091574	AI091574 ow59d04.x
45	10	33.3	44	17	AZ309736	AZ309736 1M0016L05

ALIGNMENTS

RESULT 1
AZ379320/c
LOCUS AZ379320 46 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0134P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0134P22 F, DNA sequence.
ACCESSION AZ379320
VERSION AZ379320.1 GI:10493020
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 46)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0134 row: P column: 22
 Seq primer: CCGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 46.

FEATURES

source

1. .46
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0134P22"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /note="Vector: pMD22nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 6 c 15 g 19 t
 ORIGIN
 Query Match 40.0%; Score 12; DB 17; Length 46;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ACAGAGCCCAAC 15
 Db 19 ACAGAGCCCAAC 8

RESULT 2
 BM398341
 LOCUS
 DEFINITION 5009-0-44-D05.t.2 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398341
 VERSION BM398341.1 GI:18198394
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1. 12
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"

/db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT

ORIGIN

1 a 4 c 6 g 1 t
 Query Match 36.7%; Score 11; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CGCGGTGGCAG 30
 Db 2 CGCGGTGGCAG 12

RESULT 3

BM401213

LOCUS

DEFINITION

5009-0-84-C02.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM401213

VERSION

BM401213.1 GI:18201266

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila.

ORGANISM

Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1. 19
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT

ORIGIN

3 a 5 c 8 g 3 t
 Query Match 36.7%; Score 11; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CGCGGTGGCAG 30
 Db 9 CGCGGTGGCAG 19

RESULT 4

BM395007

LOCUS

DEFINITION

50072-2-7-A08.f.2 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM395007

VERSION

BM395007.1 GI:18195060

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila.

ORGANISM

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
AUTHORS 1 (bases 1 to 20)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orian, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..20
Location/Qualifiers
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript 2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 3 a 7 c 6 g 4 t
ORIGIN

Query Match 36.7%; Score 11; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCGTGGCAG 30
|||||
Db 5 CGCGTGGCAG 15

RESULT 5
AZ781467/c
LOCUS 21 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0019F23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0019F23 R, DNA sequence.
ACCESSION AZ781467
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0019 row: F column: 23
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1..21
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="UUGC2M0019F23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 2 a 12 c 12 g 5 t
ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAA 14
|||||
Db 11 ACAGAGCCCAA 1

RESULT 6
AZ393281/c
LOCUS 22 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0156H13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0156H13 F, DNA sequence.
ACCESSION AZ393281
VERSION
KEYWORDS GSS.
SOURCE house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: H column: 13
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"

/db xref="taxon:10090"
 /clone="UUGC1M0156H13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 4 c 7 g 7 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAA 14
 |||||
 Db 21 ACAGAGCCCAA 11

RESULT 7
 AZ309564
 LOCUS
 DEFINITION 24 bp DNA linear GSS 29-SEP-2000
 1M0016E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0156E09 F, DNA sequence.
 ACCESSION
 VERSION AZ309564
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weisse,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: E column: 09
 Seq primer: CGTTGTAACGAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"

/db xref="taxon:10090"
 /clone="UUGC1M0016E09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 4 c 10 g 4 t
 ORIGIN
 Query Match 36.7%; Score 11; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCA 13
 |||||
 Db 8 GACAGAGCCCA 18

RESULT 8
 BM399150
 LOCUS
 DEFINITION 26 bp mRNA linear EST 17-JAN-2002
 5009-0-54-All.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION
 VERSION BM399150.1
 KEYWORDS GI:18199203
 SOURCE EST.
 ORGANISM Tetrahymena thermophila.
 Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 26)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: 13.
 Location/Qualifiers
 1..26
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 8 a 5 c 10 g 3 t
 ORIGIN


```

Query Match          36.7%; Score 11; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCGGGTGGCAG 30
    |||||
Db 16 CCGGGTGGCAG 26

RESULT 9
LOCUS BM398611
DEFINITION 33 bp mRNA linear EST 17-JAN-2002
5009-0-47-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398611
VERSION BM398611.1 GI:18198664
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
AUTHORS Hymenostomatida; Tetrahymena; Tetrahymena.
1 (bases 1 to 33)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. .33
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript 2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 5 a 10 c 12 g 6 t
ORIGIN

Query Match          36.7%; Score 11; DB 13; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCGGGTGGCAG 30
    |||||
Db 9 CCGGGTGGCAG 19

RESULT 10
LOCUS AL759526/c
DEFINITION 34 bp DNA linear GSS 18-JUN-2002
Arabidopsis thaliana T-DNA flanking sequence GK-188A07-014624,
genomic survey sequence.
ACCESSION AL759526
VERSION AL759526.1 GI:21497874
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
and Weisshaar, B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines
Unpublished
2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 34)
Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar, B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Atlg07990. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .34
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-188A07-014624"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
BASE COUNT 10 a 9 c 9 g 6 t
ORIGIN

Query Match          36.7%; Score 11; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCTTCGGGTG 26
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Db 13 TCTTCGGGTG 3

RESULT 11
LOCUS BJ063841
DEFINITION 37 bp mRNA linear EST 10-DEC-2001
laevis cDNA clone XL077114 5', mRNA sequence.
ACCESSION BJ063841
VERSION BJ063841.1 GI:17471031
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 37)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadabu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

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source
1. .37
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="XLO77114"
/library
/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is substracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 5 a 15 c 3 g 13 t 1 others
ORIGIN
Query Match 36.7%; Score 11; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCG 21
|||||
DB 24 CCAACTCTTCG 34

RESULT 12
LOCUS BH851915/c 40 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_073707.54.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_073707.54.25.x, DNA
sequence.
ACCESSION BH851915
VERSION BH851915.1 GI:21422786
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 40)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of AL5946110.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..40
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
BASE COUNT 7 a 11 c 12 g 10 t
ORIGIN
Query Match 36.7%; Score 11; DB 17; Length 40;

1. .37
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is substracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 5 a 15 c 3 g 13 t 1 others
ORIGIN
Query Match 36.7%; Score 11; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCG 21
|||||
DB 24 CCAACTCTTCG 34

RESULT 13
LOCUS BM400948 44 bp mRNA linear EST 17-JAN-2002
DEFINITION 5099-0-80-E05.t.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400948
VERSION BM400948.1 GI:18201001
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 44)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology

Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTCGGCGGTGGC 28
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DB 27 TTCGGCGGTGGC 17

RESULT 14
LOCUS BM397151 45 bp mRNA linear EST 17-JAN-2002
DEFINITION 5099-0-29-F01.t.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397151
VERSION BM397151.1 GI:18197204
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 45)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology

```

University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

FEATURES

source

Location/Qualifiers

1..45

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

10 a 11 c 15 g 9 t

BASE COUNT

ORIGIN

Query Match 36.7%; Score 11; DB 13; Length 45;

Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CGCGGTGGCAG 30

Db 16 CGCGGTGGCAG 26

RESULT 15

BE536289/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE536289 47 bp mRNA linear EST 09-AUG-2000

601062681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3448989 5',

mRNA sequence.

BE536289

BE536289.1 GI:9764934

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 47)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM8425 row: a column: 22

High quality sequence stop: 47.

Location/Qualifiers

1..47

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3448989"

/clone_lib="NIH_MGC_10"

/cell_line="MGC36"

/lab_host="DH10B"

/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5 kb. Library prepared by Life

Technologies."

6 a 21 c 10 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 11; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 GACAGAGCCCA 24

Search completed: June 23, 2003, 10:10:19
Job time : 1548.89 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 45.5378 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTCTTCGGGTGGCAG 30

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/prodata/2/ina/5B COMB.seq:
3: /cgn2_6/prodata/2/ina/6A COMB.seq:
4: /cgn2_6/prodata/2/ina/6B COMB.seq:
5: /cgn2_6/prodata/2/ina/6C COMB.seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	66.7	20	2	US-08-770-565-6
3	20	66.7	20	2	US-08-770-565-7
4	15.8	52.7	45	6	5198342-4
5	15.2	50.7	43	1	US-07-797-556-15
6	14.6	48.7	40	2	US-08-425-684-94
7	14.6	48.7	40	2	US-08-675-502-94
8	14.4	48.0	26	2	US-08-859-598-77
9	14.4	48.0	26	4	US-09-225-928-77
10	14.4	48.0	42	4	US-09-051-363-23
11	14.2	47.3	30	1	US-08-285-440-16
12	14.2	47.3	30	1	US-08-630-349-16
13	14.2	47.3	50	2	US-08-920-165-2
14	14	46.7	26	3	US-08-974-180-33
15	13.8	46.0	46	1	US-08-091-519-5
16	13.8	46.0	46	1	US-08-106-507-7
17	13.8	46.0	46	1	US-08-442-043A-5
18	13.8	46.0	46	5	PCT-US91-03478-5
19	13.8	46.0	47	4	US-09-338-907-222
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21	13.8	46.0	47	4	US-09-218-207-222
22	13.8	46.0	47	4	US-09-218-207-299
23	13.6	45.3	48	2	US-08-629-039-9
24	13.6	45.3	48	2	US-08-629-039-10
25	13.6	45.3	49	4	US-09-166-966B-3
26	13.4	44.7	32	2	US-08-602-264A-11
27	13.4	44.7	32	3	US-08-461-018A-11

C 28	13.4	44.7	32	4	US-09-216-958-11	Sequence 11, Appl
C 29	13.4	44.7	36	3	US-08-746-883-8	Sequence 8, Appl
C 30	13.2	44.0	30	1	US-08-484-557C-46	Sequence 46, Appl
C 31	13.2	44.0	30	1	US-08-487-426B-46	Sequence 46, Appl
C 32	13.2	44.0	30	2	US-08-487-720A-46	Sequence 46, Appl
C 33	13.2	44.0	36	3	US-08-833-167-69	Sequence 69, Appl
C 34	13.2	44.0	36	4	US-09-344-837A-69	Sequence 69, Appl
C 35	13.2	44.0	45	1	US-08-619-109-1	Sequence 1, Appl
C 36	13.2	44.0	45	2	US-08-878-166-1	Sequence 1, Appl
C 37	13.2	44.0	45	4	US-09-369-635-1	Sequence 1, Appl
C 38	13	43.3	27	1	US-08-196-538-8	Sequence 8, Appl
C 39	13	43.3	30	4	US-09-630-377-3	Sequence 3, Appl
C 40	13	43.3	37	1	US-08-217-327-15	Sequence 15, Appl
C 41	13	43.3	38	1	US-08-472-254A-23	Sequence 23, Appl
C 42	13	43.3	38	2	US-08-477-576B-23	Sequence 23, Appl
C 43	13	43.3	38	2	US-08-428-734B-23	Sequence 23, Appl
C 44	13	43.3	38	4	US-08-713-556F-23	Sequence 23, Appl
C 45	13	43.3	41	1	US-08-058-907-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-5
; Sequence 5, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-5

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Best Local Similarity 100.0%; Pred. No. 6.3e-05; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;
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1 CTGACAGAGCCCAACTCTTCGGCGTGCAG 30

Db

RESULT 2

US-08-770-565-6

Sequence 6, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-0023000US

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-7

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Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCGGGTGGCAG 30

Db 1 CCAACTCTTCGGGTGGCAG 20

RESULT 4

5198342-4

Patent No. 5198342

APPLICANT: MALIISZEWSKI, CHARLES R.

TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/548,059

FILING DATE: 05-JUL-1990

SEQ ID NO: 4:

LENGTH: 45

5198342-4

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Best Local Similarity 89.5%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GAGCCCAACTCTTCGGGT 25

Db 18 GAGGACAACTCTTCGGGT 36

RESULT 5

US-07-797-556-15/c

Sequence 15, Application US/07797556

Patent No. 5262522

GENERAL INFORMATION:

APPLICANT: Gearing, David P.

TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

1 CTGACAGAGCCCAACTCTTCGGCGTGCAG 30

Db

RESULT 2

US-08-770-565-6

Sequence 6, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-0023000US

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-6

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Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 3

US-08-770-565-7

Sequence 7, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-797-556-15

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Best Local Similarity 71.4%; Pred. No. 3e+02; 8; Indels 0; Gaps 0;
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QY 2 TGACAGAGCCCAACTCTTCGCGTGGCA 29
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RESULT 6
US-08-425-684-94/c
; Sequence 94, Application US/08425684
; Patent No. 5834252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P. C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN ESQ., TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528J-015400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-425-684-94

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Best Local Similarity 69.0%; Pred. No. 5.5e+02; 9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTCGCGTGGCAG 30
|||||
Db 36 TGAGAAAGGCCACGCTTCCCGAAGGAG 8
|||||

RESULT 7
US-08-675-502-94/c
; Sequence 94, Application US/08675502
; Patent No. 5928905
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P. C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,502
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-675-502-94

Query Match 48.7%; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.0%; Pred. No. 5.5e+02; 9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCAACTCTTCGCGTGGCAG 30
|||||
Db 36 TGAGAAAGGCCACGCTTCCCGAAGGAG 8
|||||

RESULT 8
US-08-859-998-77/c
; Sequence 77, Application US/08859998

```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/225,928
  FILING DATE: 05-Jan-1999
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/859,998
  FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Field, Bret E.
  REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-322-5070
  TELEFAX: 415-854-0875.
INFORMATION FOR SEQ ID NO: 77:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 26 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: DNA
  FEATURE:
    OTHER INFORMATION: oligonucleotide primer
    SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-225-928-77

Query Match      48.0%; Score 14.4; DB 4; Length 26;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels

OY 7 GAGCCCACTCTTCGGGTGGCAG 30
DB 24 GAGCGCCTCTCATCGCGGTAGCTG 1

RESULT 10
US-09-051-363-23/c
  Sequence 23, Application US/09051363
  Patent No. 6270993
  GENERAL INFORMATION:
    APPLICANT: Shibuya, Masabumi
    APPLICANT: Okamoto, Masaji
    APPLICANT: Niwa, Mikio
    APPLICANT: Matsumoto, Tomoe
    APPLICANT: Asano, Makoto
    APPLICANT: Segawa, Toshiaki
  TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
  NUMBER OF SEQUENCES: 24
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
  ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: Windows95
    SOFTWARE: FastSeq for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/051,363
    FILING DATE: 07-APR-1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/JP96/02906
    FILING DATE: 07-OCT-1996
    APPLICATION NUMBER: 8/211892 JP
    FILING DATE: 23-JUL-1996
    APPLICATION NUMBER: 7/296476 JP

```


;; FILING DATE: 07-OCT-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Ph.D., J.D., Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 06501/012001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: synthetic DNA
US-09-051-363-23

Query Match 48.0%; Score 14.4; DB 4; Length 42;
Best Local Similarity 93.8%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAACTCTT 19
Db 24 ACAGAGCCCAACTCTT 9

RESULT 11
US-08-285-440-16
; Sequence 16, Application US/08285440
; Patent No. 5532337
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/285,440
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/858,947
; FILING DATE: March 27, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL:
; ANTI-SENSE: Yes
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-16

Query Match 47.3%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACAGAGCCCAACTCTTCGGGTGGCAG 30
Db 2 ACCGAGCTCAAACTTAGTGGGGGAG 28

RESULT 12
US-08-630-349-16
; Sequence 16, Application US/08630349
; Patent No. 5739008
; GENERAL INFORMATION:
; APPLICANT: Ken'ichiro HAYASHI et al.
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,349
; FILING DATE: April 10, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,440
; FILING DATE: August 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/858,947

COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/091,519
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,415
 FILING DATE:
 APPLICATION NUMBER: US 07/534,193
 FILING DATE: 06-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/573,576
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/627,071
 FILING DATE: 13-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Wight, Christopher L.
 REGISTRATION NUMBER: 31680
 REFERENCE/DOCKET NUMBER: 2003-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-587-5570
 TELEFAX: 206-233-0644
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 46 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: N
 ANTI-SENSE: N
 US-08-091-519-5

Query Match 46.0%; Score 13.8; DB 1; Length 46;
 Best Local Similarity 88.2%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 9 GCCCAACTCTTCGCGT 25
 Db 21 GACAACTCTTCGCGT 37

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 Job time : 46.5378 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 91.1952 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-5
Perfect score: 30
Sequence: 1 CTGACAGAGCCCAACTCTTCGGGTGCGAG 30

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	49.3	28	9	US-10-151-320-25
2	14.6	48.7	40	10	US-09-245-802-94
3	14.4	48.0	19	9	US-10-093-958-22
4	14.4	48.0	31	10	US-09-801-274-373
5	13.8	46.0	27	9	US-09-733-634-11
6	13.8	46.0	46	9	US-10-199-209-5
7	13.8	46.0	47	9	US-09-853-526-222
8	13.8	46.0	47	9	US-09-853-526-299
9	13.8	46.0	47	10	US-09-901-484A-222
10	13.8	46.0	47	10	US-09-901-484A-299
11	13.6	45.3	24	10	US-09-820-339A-23
12	13.6	45.3	28	9	US-10-152-363A-48
13	13.6	45.3	29	9	US-10-152-363A-41
14	13.6	45.3	29	9	US-10-152-363A-42
15	13.6	45.3	48	9	US-10-152-363A-16
16	13.4	44.7	21	9	US-09-909-567B-23
17	13.4	44.7	23	10	US-09-766-154-31
18	13.4	44.7	25	9	US-10-098-263B-5571
19	13.4	44.7	25	9	US-10-098-263B-47598

20 13.4 44.7 25 9 US-10-098-263B-79874 Sequence 79874, A
c 21 13.4 44.7 25 9 US-10-098-263B-84572 Sequence 84572, A
c 22 13.4 44.7 32 10 US-09-866-712-11 Sequence 11, Appl
c 23 13.4 44.7 33 9 US-10-006-591-8 Sequence 8, Appl
24 13.4 44.7 35 9 US-10-216-484-86 Sequence 86, Appl
25 13.4 44.7 50 9 US-09-978-295A-83 Sequence 83, Appl
26 13.4 44.7 50 9 US-09-978-697-83 Sequence 83, Appl
27 13.4 44.7 50 9 US-09-978-192A-83 Sequence 83, Appl
28 13.4 44.7 50 9 US-09-999-832A-83 Sequence 83, Appl
29 13.4 44.7 50 9 US-09-978-189-83 Sequence 83, Appl
30 13.4 44.7 50 9 US-09-978-608A-83 Sequence 83, Appl
31 13.4 44.7 50 9 US-09-978-191A-83 Sequence 83, Appl
32 13.4 44.7 50 9 US-09-978-403A-83 Sequence 83, Appl
33 13.4 44.7 50 9 US-09-978-564A-83 Sequence 83, Appl
34 13.4 44.7 50 9 US-09-978-585A-83 Sequence 83, Appl
35 13.4 44.7 50 9 US-10-017-081A-83 Sequence 83, Appl
36 13.4 44.7 50 9 US-09-978-824-83 Sequence 83, Appl
37 13.4 44.7 50 9 US-09-981-915A-83 Sequence 83, Appl
38 13.4 44.7 50 9 US-09-999-833A-83 Sequence 83, Appl
39 13.4 44.7 50 9 US-10-167-749-83 Sequence 83, Appl
40 13.4 44.7 50 9 US-09-918-585A-83 Sequence 83, Appl
41 13.4 44.7 50 9 US-09-978-423A-83 Sequence 83, Appl
42 13.4 44.7 50 9 US-10-013-921A-83 Sequence 83, Appl
43 13.4 44.7 50 9 US-09-978-193A-83 Sequence 83, Appl
44 13.4 44.7 50 9 US-10-013-929A-83 Sequence 83, Appl
45 13.4 44.7 50 9 US-10-016-177A-83 Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-10-151-320-25
; Sequence 25, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436
; CURRENT APPLICATION NUMBER: US/10/151,320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer used for PCR.
US-10-151-320-25

Query Match 49.3%; Score 14.8; DB 9; Length 28;
Best Local Similarity 73.1%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTCGGGTG 26
||||| ||||| ||||| |||||

Db 1 CTGGCCAGCCCAACTCTTCAGCTG 26
||||| ||||| ||||| |||||

RESULT 2
US-09-245-802-94/c
; Sequence 94, Application US/09245802
; Patent No. US20010049125A1
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSCHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: U.S.A.
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/245,802
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/675,502
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05480
 FILING DATE: 18-APR-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY, ESQ., MATTHEW B.
 REGISTRATION NUMBER: 39,787
 REFERENCE/DOCKET NUMBER: 16528J-015410US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 US-09-245-802-94

Query Match 48.7%; Score 14.6; DB 10; Length 40;
 Best Local Similarity 69.0%; Pred. No. 2.4e+03;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCACTCTTCGCGTGGCAG 30
 DB 36 TGAGAAAGCGCCAGCTTCCGGAAGGAG 8

RESULT 3
 US-10-093-958-22
 ; Sequence 22, Application US/10093958
 ; Publication No. US2003004423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gillies, Stephen
 ; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
 ; FILE REFERENCE: LEX-016
 ; CURRENT APPLICATION NUMBER: US/10/093,958
 ; PRIOR FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 60/274,096
 ; PRIOR FILING DATE: 2001-03-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: forward primer for gamma 1 hinge region
 US-10-093-958-22

Query Match 48.0%; Score 14.4; DB 9; Length 19;
 Best Local Similarity 93.8%; Pred. No. 3e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTCTTC 20
 DB 4 CAGAGCCCACTCTTC 19

RESULT 4
 US-09-801-274-373/c
 ; Sequence 373, Application US/09801274
 ; Patent No. US20020032319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Lander, Eric S.
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: 2825-2009-001
 ; CURRENT APPLICATION NUMBER: US/09/801,274
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/187,510
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 60/206,129
 ; PRIOR FILING DATE: 2000-05-22
 ; NUMBER OF SEQ ID NOS: 1802
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 373
 ; LENGTH: 31
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-801-274-373

Query Match 48.0%; Score 14.4; DB 10; Length 31;
 Best Local Similarity 69.2%; Pred. No. 2.9e+03;
 Matches 18; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 CAGAGCCCACTCTTCGCGTGGCAG 30
 DB 27 CAGAGCCCACTCTTCGCGTGGCAG 2

RESULT 5
 US-09-733-634-11/c
 ; Sequence 11, Application US/09733634
 ; Publication No. US20030013646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Massachusetts General Hospital
 ; TITLE OF INVENTION: Method to stimulate Insulin production by pancreatic b-cells
 ; FILE REFERENCE: 17633/1240
 ; CURRENT APPLICATION NUMBER: US/09/733,634
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: US 60/170,282
 ; PRIOR FILING DATE: 1999-12-10
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 11
 ; LENGTH: 27
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic primer
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)..(27)
 ; OTHER INFORMATION: Synthetic primer
 US-09-733-634-11

Query Match 46.0%; Score 13.8; DB 9; Length 27;
 Best Local Similarity 72.0%; Pred. No. 5.5e+03;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTCGCGGT 25
 DB 26 CTGACAGAGCCCACTCTTCGCGGT 2

RESULT 6

US-10-199-209-5
; Sequence 5, Application US/10199209
; Publication No. US20030060616A1
; GENERAL INFORMATION:
; APPLICANT: Sina, John E.
; Cosman, David J.
; Lupton, Stephen D.
; Mosley, Bruce A.
; Dower, Steven K.
; TITLE OF INVENTION: Type II Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,209
; FILING DATE: 19-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,908
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/091,519
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/701,415
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/534,193
; FILING DATE: 06-JUN-1990
; APPLICATION NUMBER: US 07/573,576
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: US 07/627,071
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31680
; REFERENCE/DOCKET NUMBER: 2003-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-5570
; TELEFAX: 206-233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-199-209-5

Query Match 46.0%; Score 13.8; DB 9; Length 46;
Best Local Similarity 88.2%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTCGCGGT 25
Db 21 GACAAACTCTTCGCGGT 37

RESULT 7

US-09-853-526-222/c
; Sequence 222, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 222
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: polymorphic fragment 4-84-241
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 4-84-241.mis1
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-853-526-222

Query Match 46.0%; Score 13.8; DB 9; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCACTCTTCGCGTGGCAG 30
Db 41 AGAACTGAATTATTCACCGTGGCAG 17

RESULT 8

US-09-853-526-299/c
; Sequence 299, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 299
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens

Query Match 46.0%; Score 13.8; DB 9; Length 46;
Best Local Similarity 88.2%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCCCAACTCTTCGCGGT 25
Db 21 GACAAACTCTTCGCGGT 37

RESULT 7

US-09-853-526-222/c
; Sequence 222, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:

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FEATURE:
NAME/KEY: allele
LOCATION: 1..47
OTHER INFORMATION: polymorphic fragment 4-84-241, variant version of SEQ ID222
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: base T ; G in SEQ ID222
NAME/KEY: primer_bind
LOCATION: 1..23
OTHER INFORMATION: potential microsequencing oligo 4-84-241.misl
NAME/KEY: primer_bind
LOCATION: 25..47
OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-853-526-299

Query Match          46.0%; Score 13.8; DB 9; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 9
US-09-901-484A-222/c
Sequence 222, Application US/09901484A
Patent No. US20020119460A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
FILE REFERENCE: GEN-T11XC3D2
CURRENT APPLICATION NUMBER: US 09/901,484A
PRIOR FILING DATE: 2001-07-09
CURRENT APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: US 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/853,526
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent in version 3.1
SEQ ID NO 222
LENGTH: 47
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1)..(47)
OTHER INFORMATION: polymorphic fragment 4-84-241, variant version of SEQ ID 222
CURRENT APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: US 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/853,526
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent in version 3.1
SEQ ID NO 222
LENGTH: 47
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1)..(47)
OTHER INFORMATION: polymorphic fragment 4-84-241
NAME/KEY: allele
LOCATION: (24)..(24)
OTHER INFORMATION: polymorphic base G
NAME/KEY: primer_bind
LOCATION: (1)..(23)
OTHER INFORMATION: potential microsequencing oligo 4-84-241.misl
NAME/KEY: primer_bind
LOCATION: (25)..(47)
OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-901-484A-222

Query Match          46.0%; Score 13.8; DB 10; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 11
US-09-820-339A-23/c
Sequence 23, Application US/09820339A
Patent No. US20020081652A1
GENERAL INFORMATION:
APPLICANT: FUCHS, Sara
APPLICANT: BARCHAN, Dora
APPLICANT: SOUROUJON, Miriam
TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND TH-
FILE REFERENCE: FUCHS=2A
CURRENT APPLICATION NUMBER: US/09/820,339A
PRIOR FILING DATE: 1999-11-08
CURRENT APPLICATION NUMBER: 09/423,398
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: PCT/IL98/00211
US-09-901-484A-222

Query Match          46.0%; Score 13.8; DB 10; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17
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Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 10
US-09-901-484A-299/c
Sequence 299, Application US/09901484A
Patent No. US20020119460A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
FILE REFERENCE: GEN-T11XC3D2
CURRENT APPLICATION NUMBER: US/09/901,484A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: US 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: US 09/853,526
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent in version 3.1
SEQ ID NO 299
LENGTH: 47
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1)..(47)
OTHER INFORMATION: polymorphic fragment 4-84-241, variant version of SEQ ID 222
NAME/KEY: allele
LOCATION: (24)..(24)
OTHER INFORMATION: polymorphic base T; G in SEQ ID 222
NAME/KEY: primer_bind
LOCATION: (1)..(23)
OTHER INFORMATION: potential microsequencing oligo 4-84-241.misl
NAME/KEY: primer_bind
LOCATION: (25)..(47)
OTHER INFORMATION: complement potential microsequencing oligo 4-84-241.mis2
US-09-901-484A-299

Query Match          46.0%; Score 13.8; DB 10; Length 47;
Best Local Similarity 72.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 AGAGCCCAACTCTTCGGGTGGCAG 30
Db 41 AGAAGTGAATTATTCACAGTGGCAG 17

RESULT 11
US-09-820-339A-23/c
Sequence 23, Application US/09820339A
Patent No. US20020081652A1
GENERAL INFORMATION:
APPLICANT: FUCHS, Sara
APPLICANT: BARCHAN, Dora
APPLICANT: SOUROUJON, Miriam
TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND TH-
FILE REFERENCE: FUCHS=2A
CURRENT APPLICATION NUMBER: US/09/820,339A
PRIOR FILING DATE: 1999-11-08
CURRENT APPLICATION NUMBER: 09/423,398
PRIOR FILING DATE: 1999-11-08
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Best Local Similarity 80.0%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Job time : 92.1952 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 2545.58 Seconds
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Perfect score: 30
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SUMMARIES

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LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 16"
PCT-US97-23619-5

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30

RESULT 2
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; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-5

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30
DB 1 CTGACAGAGCCCACTCTTCGGGTGGCAG 30

RESULT 3
US-08-521-634-15/c

Sequence 62082, A
Sequence 16215, A
Sequence 16228, A
Sequence 992959, A
Sequence 187, App
Sequence 40536, A
Sequence 301573, A
Sequence 809390, A
Sequence 207601, A
Sequence 28958, A
Sequence 3806, App
Sequence 26072, A
Sequence 141444, A
Sequence 141444, A
Sequence 141444, A
Sequence 134580, A
Sequence 592670, A
Sequence 5017, App
Sequence 25, Appl
Sequence 25, Appl
Sequence 2846, App
Sequence 38072, A
Sequence 24820, A

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; Sequence 15, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-521-634-15

Query Match 80.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACAGAGCCCAACTCTTCGCGGTG 26
Db 24 GACAGAGCCCAACTCTTCGCGGTG 1

RESULT 4
PCT-US97-23619-6
; Sequence 6, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase

; Sequence 7, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

; Sequence 15, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..20
; OTHER INFORMATION: /note= "oligo 16ab"
; PCT-US97-23619-6

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 5
PCT-US97-23619-7
; Sequence 7, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..20
; OTHER INFORMATION: /note= "oligo 16bc"
; PCT-US97-23619-7

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCGCGGTGGCAG 30
Db 1 CCAACTCTTCGCGGTGGCAG 20

RESULT 6
US-08-770-564A-6
; Sequence 6, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US97-23619-7

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-6

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 7
US-08-770-564A-7
; Sequence 7, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-7

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCAACTCTTCGCGGTGGCAG 30
Db 1 CCAACTCTTCGCGGTGGCAG 20

RESULT 8

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US-09-956-604-105231/c
; Sequence 105231, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-105231

Query Match          61.3%; Score 18.4; DB 36; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 9
US-09-956-604A-105231/c
; Sequence 105231, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604A-105231

Query Match          61.3%; Score 18.4; DB 36; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 10
US-09-956-604B-105231/c
; Sequence 105231, Application US/09956604B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604B
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604B-105231
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Query Match          61.3%; Score 18.4; DB 36; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 11
US-60-234-049-86453/c
; Sequence 86453, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-86453

Query Match          61.3%; Score 18.4; DB 67; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCCAACTCTTCGGGTGGCA 29
Db 23 CACAACTCTTCGGGTGGCA 4

RESULT 12
US-09-404-520-39034/c
; Sequence 39034, Application US/09404520
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodssi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 39034
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-39034

Query Match          60.0%; Score 18; DB 18; Length 48;
Best Local Similarity 80.8%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTCGGGTGGCAG 30
Db 33 CAGAGCCCAAGCTCATGGCGGCGCAG 8

RESULT 13
US-09-404-520-37700/c
; Sequence 37700, Application US/09404520
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```
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodessi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 3700
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
; US-09-404-520-37700

Query Match          57.3%; Score 17.2; DB 18; Length 41;
Best Local Similarity 73.3%; Pred. No. 4e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTCGGCGGTGGCAG 30
Db      37 CGGACATAGACCAACACATGGCGCGGCAG 8

RESULT 14
US-60-353-790-1064
; Sequence 1064, Application US/60353790
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0235 PSP
; CURRENT APPLICATION NUMBER: US/60/353,790
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3792
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1064
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-353-790-1064

Query Match          57.3%; Score 17.2; DB 79; Length 41;
Best Local Similarity 73.3%; Pred. No. 4e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CTGACAGAGCCCAACTCTTCGGCGGTGGCAG 30
Db      8 CCGTGAGAGTCCAACCTCTGCCCTGGGGCAG 37

RESULT 15
PCT-US01-47856-7470/c
; Sequence 7470, Application PC/TUS0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Quertermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7470
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human adenovirus type 2
; PCT-US01-47856-7470

Query Match          56.7%; Score 17; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      6 AGAGCCCAACTCTTCGGCGGTGGCAG 30
Db      31 AGAGCCCAACTCAGCGCGGTGGCAG 7

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 21.2789 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
10: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	10	9	US-09-988-462-49
2	7	100.0	10	10	US-09-816-763-61
3	7	100.0	10	12	US-10-033-145-226
4	7	100.0	10	12	US-10-033-145-1449
5	7	100.0	11	9	US-09-249-155-34
6	7	100.0	13	9	US-09-879-813-84
7	7	100.0	13	9	US-10-146-505-84
8	7	100.0	13	10	US-09-770-601-4
9	7	100.0	13	10	US-09-770-601-6
10	7	100.0	14	9	US-10-146-058-41
11	7	100.0	15	9	US-10-146-575-21
12	7	100.0	15	9	US-10-145-289-2
13	7	100.0	15	10	US-09-922-261-10
14	7	100.0	16	9	US-10-146-058-39
15	7	100.0	17	9	US-09-879-813-51
16	7	100.0	17	9	US-10-041-856-79
17	7	100.0	17	9	US-09-780-164-249
18	7	100.0	17	9	US-09-780-164-250
19	7	100.0	17	9	US-09-780-164-612

Sequence 613, App
Sequence 738, App
Sequence 825, App
Sequence 928, App
Sequence 1066, App
Sequence 6, Appli
Sequence 7, Appli
Sequence 248, App
Sequence 250, App
Sequence 251, App
Sequence 252, App
Sequence 253, App
Sequence 254, App
Sequence 255, App
Sequence 256, App
Sequence 257, App
Sequence 258, App
Sequence 1537, App
Sequence 1538, App
Sequence 1539, App
Sequence 1540, App
Sequence 1541, App
Sequence 1542, App
Sequence 1543, App
Sequence 1544, App

ALIGNMENTS

RESULT 1

US-09-988-462-49
Sequence 49, Application US/09988462
Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NOV-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-988-462-49

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 2

US-09-816-763-61
; Sequence 61, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: ISGF3
US-09-816-763-61

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 1 GCTTCAG 7

RESULT 3

US-10-033-145-226/c
; Sequence 226, Application US/10033145
; Patent No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS

; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-226

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 9 GCTTCAG 3

RESULT 4

US-10-033-145-1449/c
; Sequence 1449, Application US/10033145
; Patent No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1449

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 10 GCTTCAG 4

RESULT 5

US-09-249-155-34/c
; Sequence 34, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 34
LENGTH: 11
TYPE: DNA
ORGANISM: Mus musculus
US-09-249-155-34

Query Match 100.0%; Score 7; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
DB 10 GCTTCAG 4

RESULT 6

US-09-879-813-84/c
Sequence 84, Application US/09879813
Patent No. US20020155453A1
GENERAL INFORMATION:
APPLICANT: Neuberger, Julian E.
APPLICANT: Neuberger, Michael S.
APPLICANT: Cumbers, Sarah J.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005
CURRENT APPLICATION NUMBER: US/09/879,813
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/828,717
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: PCT/GB99/03358
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.1
SEQ ID NO 84
LENGTH: 13
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (8)..(8)
OTHER INFORMATION: F220
OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-09-879-813-84

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
DB 7 GCTTCAG 1

RESULT 7

US-10-146-505-84/c
Sequence 84, Application US/10146505
Publication No. US20030108889A1
GENERAL INFORMATION:
APPLICANT: Sale, Julian E.
APPLICANT: Neuberger, Michael S.
APPLICANT: Cumbers, Sarah J.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005B
CURRENT APPLICATION NUMBER: US/10/146,505
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/828,717
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 09/879,813
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: PCT/GB99/03358
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: GB 9822104.7
PRIOR FILING DATE: 1998-10-09

PRIOR APPLICATION NUMBER: GB 9901141.3
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: GB 9913435.5
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn version 3.1
SEQ ID NO 84
LENGTH: 13
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (8)..(8)
OTHER INFORMATION: F220
OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-10-146-505-84

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
DB 7 GCTTCAG 1

RESULT 8

US-09-770-601-4
Sequence 4, Application US/09770601
Patent No. US20020104110A1
GENERAL INFORMATION:
APPLICANT: Lipes, Myra A.
APPLICANT: Chen, Qian
TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
FILE REFERENCE: 10276-015002
CURRENT APPLICATION NUMBER: US/09/770,601
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/127,276
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: 60/054,730
PRIOR FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer for PCR
US-09-770-601-4

Query Match 100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
DB 7 GCTTCAG 13

RESULT 9

US-09-770-601-6/c
Sequence 6, Application US/09770601
Patent No. US20020104110A1
GENERAL INFORMATION:
APPLICANT: Lipes, Myra A.
APPLICANT: Chen, Qian
TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
FILE REFERENCE: 10276-015002
CURRENT APPLICATION NUMBER: US/09/770,601
CURRENT FILING DATE: 2001-01-26

;; PRIOR APPLICATION NUMBER: 09/127,276
;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: 60/054,730
;; PRIOR FILING DATE: 1997-08-05
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 13
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: primer for PCR
US-09-770-601-6

Query Match 100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAG 7
Db 7 GCCTCAG 1

RESULT 10
US-10-146-058-41/c
; Sequence 41, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: YES
US-10-146-058-41

Query Match 100.0%; Score 7; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAG 7
Db 11 GCCTCAG 5

RESULT 11
US-10-146-575-21/c
; Sequence 21, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-146-575-21

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTCAG 7
Db 8 GCCTCAG 2

RESULT 12
US-10-145-289-2
; Sequence 2, Application US/10145289
; Publication No. US20030077812A1
; GENERAL INFORMATION:
; APPLICANT: James G. McArthur
; APPLICANT: Dale John Talbot
; APPLICANT: Andrew D. Simmons
; APPLICANT: Ryan McGuinness
; APPLICANT: Michael Kelly
; APPLICANT: Lisa V. Tsui
; APPLICANT: Thomas Dull
; TITLE OF INVENTION: LENTIVIRAL VECTORS ENCODING CLOTTING
; TITLE OF INVENTION: FACTORS FOR GENE THERAPY
; FILE REFERENCE: 131.2USU1
; CURRENT APPLICATION NUMBER: US/10/145,289
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/291,083
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-289-2

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Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      9 GCTTCAG 15

RESULT 13
US-09-922-261-10/c
; Sequence 10, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 1001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-261-10

Query Match      100.0%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      11 GCTTCAG 5

RESULT 14
US-10-146-058-39/c
; Sequence 39, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-39

Query Match      100.0%; Score 7; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      7 GCTTCAG 1

RESULT 15
US-09-879-813-51/c
; Sequence 51, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(12)
; OTHER INFORMATION: D3
; OTHER INFORMATION: The sequence GACCC between positions 7 and 12 replace the sequence
; OTHER INFORMATION: e AGGACTGT
US-09-879-813-51

Query Match      100.0%; Score 7; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
Db      11 GCTTCAG 7
```

Db 17 GCTTCAG 11

Search completed: June 25, 2003, 22:25:08
Job time : 21.2789 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 22.7689 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	2	US-08-770-565-10
2	15	100.0	19	2	US-08-770-565-9
3	15	100.0	26	1	US-08-330-123A-23
4	15	100.0	26	1	US-08-482-115B-23
5	15	100.0	26	2	US-08-660-678A-23
6	15	100.0	26	2	US-08-710-249-26
7	15	100.0	26	2	US-08-485-778-19
8	15	100.0	26	2	US-08-472-802C-24
9	15	100.0	26	3	US-08-520-550A-19
10	15	100.0	26	3	US-08-998-443-23
11	15	100.0	26	4	US-08-974-549A-598
12	15	100.0	26	4	US-09-060-523-23
13	15	100.0	26	4	US-09-220-157A-26
14	15	100.0	26	4	US-09-286-959B-4
15	15	100.0	26	4	US-09-580-517-23
16	15	100.0	27	2	US-08-770-565-26
17	15	100.0	30	2	US-08-770-565-8
18	14	93.3	27	3	US-08-630-172-24
19	14	93.3	27	4	US-09-375-419-24
20	14	93.3	30	2	US-08-833-377-6
21	13.4	89.3	18	4	US-08-974-549A-543
22	12.4	82.7	23	4	US-09-273-839A-3
23	12.4	82.7	26	1	US-08-480-604A-16
24	12.4	82.7	26	2	US-08-405-496A-16
25	12.4	82.7	26	4	US-08-915-136-16
26	12.4	82.7	26	4	US-08-957-310-16
27	12.4	82.7	33	3	US-08-630-172-22

28	12.4	82.7	33	4	US-09-375-419-22	Sequence 22, Appl
29	12.4	82.7	40	1	US-08-395-800A-12	Sequence 12, Appl
30	12.4	82.7	42	1	US-08-439-813-2	Sequence 2, Appl
31	12.4	82.7	42	5	PCT-US96-05291A-2	Sequence 2, Appl
32	12	80.0	30	1	US-08-349-006-3	Sequence 3, Appl
33	12	80.0	30	5	PCT-US94-02107-3	Sequence 3, Appl
34	11.8	78.7	24	2	US-09-258-257-3	Sequence 3, Appl
35	11.8	78.7	24	2	US-09-258-371-3	Sequence 3, Appl
36	11.8	78.7	24	3	US-08-569-721A-3	Sequence 3, Appl
37	11.8	78.7	24	3	US-08-751-230-3	Sequence 3, Appl
38	11.8	78.7	24	3	US-09-499-082-3	Sequence 3, Appl
39	11.8	78.7	24	4	US-09-258-372-3	Sequence 3, Appl
c 40	11.8	78.7	26	2	US-09-258-257-4	Sequence 4, Appl
c 41	11.8	78.7	26	2	US-09-258-371-4	Sequence 4, Appl
c 42	11.8	78.7	26	3	US-08-569-721A-4	Sequence 4, Appl
c 43	11.8	78.7	26	3	US-08-751-230-4	Sequence 4, Appl
c 44	11.8	78.7	26	3	US-09-499-082-4	Sequence 4, Appl
c 45	11.8	78.7	26	4	US-09-258-372-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-10
; Sequence 10, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-10

Query Match 100.0% Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 7.8; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 1 GCTCTAGATGAACG 15
|||
US-08-770-565-9
Sequence 9, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-9
Query Match 100.0%; Score 15; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACG 15
Db 1 GCTCTAGATGAACG 15
|||
RESULT 3
US-08-330-123A-23
Sequence 23, Application US/08330123A
Patent No. 5583016
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23
Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19
|||
RESULT 4
US-08-482-115B-23
Sequence 23, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACG 15
DB 5 GCTCTAGTAATGAACG 19

RESULT 5
US-08-660-678A-23
Sequence 23, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Vilpeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-660-678A-23

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACG 15
DB 5 GCTCTAGTAATGAACG 19

RESULT 6
US-08-710-249-26
Sequence 26, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Vilpeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,249
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/583,808
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGTAATGAACG 15
DB 5 GCTCTAGTAATGAACG 19

RESULT 7
US-08-485-778-19
Sequence 19, Application US/08485778

```
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 9
US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995

Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 8
US-08-472-802C-24
Sequence 24, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
```

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-9540
; TELEFAX: 617-861-6240
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-520-550A-19

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 10
US-08-998-443-23
; Sequence 23, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-998-443-23

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 11
US-08-974-549A-598
; Sequence 598, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
|||||
Db 5 GCTCTAGATGAACG 19

RESULT 12
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
|||||
Db 5 GCTCTAGATGAACG 19

RESULT 13
US-09-220-157A-26
Sequence 26, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,157A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-220-157A-26

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

RESULT 14
US-09-286-959B-4
; Sequence 4, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-286-959B-4

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

RESULT 15
US-09-580-517-23
; Sequence 23, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,517
; FILING DATE: 25-May-2000
; CLASSIFICATION: <Unknown>
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,123
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
   |||||
DB 5 GCTCTAGATGAACG 19

Search completed: June 25, 2003, 00:24:39
Job time : 22.7689 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 773.367 Seconds

(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15

Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10	66.7	19	17	AZ471573
C 2	10	66.7	29	17	TA264G10Q
C 3	10	66.7	34	10	AV964763
C 4	10	66.7	49	17	BH791685
C 5	9	60.0	22	9	AU259636
C 6	9	60.0	25	9	AI763346

C	7	9	60.0	27	9	AU254302
	8	9	60.0	27	17	BH812447
	9	9	60.0	27	17	BH849811
	10	9	60.0	27	17	TA349B02P
	11	9	60.0	28	17	TA116E03P
	12	9	60.0	30	9	AU257604
C	13	9	60.0	31	9	A1032592
	14	9	60.0	34	12	BG339578
	15	9	60.0	34	12	BG340055
	16	9	60.0	36	12	BE797241
	17	9	60.0	36	17	AZ812974
C	18	9	60.0	38	17	AZ786040
C	19	9	60.0	40	12	BG563012
	20	9	60.0	41	9	AU258962
C	21	9	60.0	41	17	AZ775318
	22	9	60.0	41	17	BH863752
C	23	9	60.0	41	17	BH863753
C	24	9	60.0	41	17	BH864990
C	25	9	60.0	42	12	BF732142
C	26	9	60.0	42	12	BG613445
C	27	9	60.0	42	14	C01062
C	28	9	60.0	43	9	AA445326
	29	9	60.0	43	17	AZ456311
	30	9	60.0	44	17	AZ435397
	31	9	60.0	44	17	BH624958
C	32	9	60.0	44	17	AL757115
C	33	9	60.0	46	17	AZ812338
C	34	9	60.0	46	17	AL771310
C	35	9	60.0	46	17	TA114E02P
C	36	9	60.0	48	17	AZ831830
C	37	9	60.0	49	10	AW100845
C	38	9	60.0	50	9	AU103413
C	39	9	60.0	50	9	AU105700
C	40	9	60.0	50	14	BH889496
C	41	9	60.0	50	17	AZ478817
C	42	8	53.3	18	14	BQ790001
C	43	8	53.3	19	17	AZ309082
C	44	8	53.3	19	17	AZ659092
C	45	8	53.3	21	14	TI7609

ALIGNMENTS

RESULT 1
AZ471573/c
LOCUS
DEFINITION
AZ471573
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

19 bp DNA linear GSS 04-OCT-2000
mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0286G13 F, DNA sequence.
GI:10629698
house mouse.
Mus musculus
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0286 row: G column: 13
 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286G13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 3 c 6 g 4 t
 ORIGIN
 Query Match 66.7%; Score 10; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 CTCTAGATG 11
 Db 15 CTCTAGATG 6
 RESULT 2
 TA264G10Q 29 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION
 T. brucei sheared genomic DNA clone 264g10, reverse sequence, genomic survey sequence.
 ACCESSION
 AL487013.1 GI:11850630
 VERSION
 AL487013.1
 KEYWORDS
 GSS.
 SOURCE
 Trypanosoma brucei.
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 29)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
 1. .29
 Location/Qualifiers
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="264g10"
 11 a 5 c 11 g 2 t

BASE COUNT

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 3.6e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 AGAATGAACG 15
 Db 7 AGAATGAACG 16

RESULT 3
 AV964763/c 34 bp mRNA linear EST 14-MAR-2002
 LOCUS
 DEFINITION
 AV964763 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciadi506 5', mRNA sequence.
 ACCESSION
 AV964763
 VERSION
 AV964763.1 GI:19454459
 KEYWORDS
 EST.
 SOURCE
 Ciona intestinalis.
 Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
 1 (bases 1 to 34)
 Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Ciona intestinalis
 Unpublished (2000)
 Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.
 Location/Qualifiers
 1. .34
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ciadi506"
 /clone_lib="Nori Satoh unpublished cDNA library, young adult."
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT

ORIGIN
 Query Match 66.7%; Score 10; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

RESULT 4

BH791685
 LOCUS
 DEFINITION
 BH791685
 SALK 060837.45.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_060837.45.60.x, DNA sequence.

BASE COUNT

ORIGIN
 Query Match 66.7%; Score 10; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

RESULT 4

BH791685
 LOCUS
 DEFINITION
 BH791685
 SALK 060837.45.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_060837.45.60.x, DNA sequence.

BASE COUNT

ORIGIN
 Query Match 66.7%; Score 10; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1. .34
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ciadi506"
 /clone_lib="Nori Satoh unpublished cDNA library, young adult."
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1. .34
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ciadi506"
 /clone_lib="Nori Satoh unpublished cDNA library, young adult."
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT

ORIGIN
 Query Match 66.7%; Score 10; DB 10; Length 34;
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 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
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 /organism="Ciona intestinalis"
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 /dev_stage="young adult"
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BASE COUNT

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 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1. .34
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ciadi506"
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 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
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 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 /clone="ciadi506"
 /clone_lib="Nori Satoh unpublished cDNA library, young adult."
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT

ORIGIN
 Query Match 66.7%; Score 10; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
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 /organism="Ciona intestinalis"
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 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

BASE COUNT

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 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGAT 10
 Db 16 GCTCTAGAT 7

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

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 /db_xref="taxon:7719"
 /clone="ciadi506"
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 /tissue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector: pBluescript SK"

ACCESSION BH791685
 VERSION BH791685.1 GI:19885809
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 thale cress.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 49)
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 AUTHORS C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 FEATURES
 source
 1. .49
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="SALK_060837.45.60.x"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 15 a 9 c 9 g 16 t
 BASE COUNT
 ORIGIN
 Query Match 66.7%; Score 10; DB 17; Length 49;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAAT 10
 Db 39 GCTCTAGAAT 48
 RESULT 5
 AU259636
 LOCUS AU259636 3'-directed mouse cDNA library Mus musculus cDNA clone
 DEFINITION BED0015510 3', mRNA sequence.
 ACCESSION AU259636
 VERSION AU259636.1 GI:20326342
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 REFERENCE Kato,K. and Matoba,R.
 AUTHORS Generation of expressed sequence tags from mouse brain
 TITLE Unpublished (2002)
 JOURNAL Contact: Kikuya Kato
 COMMENT Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkatob@bs.aist-nara.ac.jp.

URL:<http://love2.aist-nara.ac.jp/BED/index.html>.
 Location/Qualifiers
 1. .22
 /organism="Mus musculus"
 /db_xref="taxon:10090"
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 /tissue type="brain"
 /note="Vector: pGEM-T-easy"
 13 a 3 c 4 g 2 t
 BASE COUNT
 ORIGIN
 Query Match 60.0%; Score 9; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 AGAATGAAC 14
 Db 11 AGAATGAAC 19
 RESULT 6
 AU259636
 LOCUS AU259636 25 bp mRNA linear EST 21-DEC-1999
 DEFINITION wi55d06.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:2394155 3',
 similar to TR:O75053 KIAA0465 PROTEIN ;, mRNA sequence.
 ACCESSION AU259636
 VERSION AU259636.1 GI:5179013
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 25)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1675 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .25
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2394155"
 /clone_lib="NCI CGAP Co16"
 /tissue type="colon tumor, RER+"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a
 modified polylinker; Site 1: Not 1; Site 2: ECO RI;
 Plasmid DNA from the normalized library NCI CGAP Co10 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneIDs 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 9 a 3 c 7 g 6 t
 BASE COUNT
 ORIGIN
 Query Match 60.0%; Score 9; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTAGATGA 12
 |||||
 Db 12 CTAGATGA 20

RESULT 7
 AU254302/c 27 bp mRNA linear EST 25-APR-2002
 LOCUS AU254302 3'-directed mouse cDNA library Mus musculus cDNA clone
 DEFINITION BED0001498 3', mRNA sequence.

ACCESSION AU254302
 VERSION AU254302.1 GI:20315955
 KEYWORDS EST.
 ORGANISM Mus musculus
 SOURCE house mouse.
 COMMENT Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Kato, K. and Matsuda, R.
 TITLE Generation of expressed sequence tags from mouse brain
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkatob@bs.aist-nara.ac.jp,
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
 source Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="BED0001498"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue_type="brain"
 /note="Vector: pGEM-T-easy"
 BASE COUNT 11 a 3 c 4 g 9 t
 ORIGIN

Query Match 60.0%; Score 9; DB 9; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TAGAATGAA 13
 |||||
 Db 25 TAGAATGAA 17

RESULT 8
 BH812447 27 bp DNA linear GSS 02-MAY-2002
 LOCUS BH812447
 DEFINITION SALK_061781 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_061781, DNA sequence.

ACCESSION BH812447
 VERSION BH812447.1 GI:20390902
 KEYWORDS GSS.
 ORGANISM Arabidopsis thaliana
 SOURCE thale cress.
 COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
 C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

Class: TDNA tagged.
 Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_061781"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 BASE COUNT 12 a 3 c 5 g 7 t
 ORIGIN

Query Match 60.0%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTAGAT 10
 |||||
 Db 18 CTCTAGAT 26

RESULT 9
 BH849811 27 bp DNA linear GSS 13-JUN-2002
 LOCUS BH849811
 DEFINITION SALK_070310.38.90.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_070310.38.90.x, DNA
 sequence.

ACCESSION BH849811
 VERSION BH849811.1 GI:21420682
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
 C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

Class: TDNA tagged.
 Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_070310.38.90.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT
ORIGIN

7 a 2 c 8 g 10 t

Query Match 60.0%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATG 11
|||||
Db 8 TCTAGATG 16

RESULT 10
TA349B02P 27 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 349b02, forward sequence,
genomic survey sequence.

ACCESSION
AL493641

VERSION
AL493641.1 GI:11869420

KEYWORDS

SOURCE
Trypanosoma brucei.

ORGANISM
Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE
1 (bases 1 to 27)

AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

JOURNAL

COMMENT
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source

1. .27
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="349b02"

BASE COUNT 4 a 10 c 8 g 5 t

Query Match 60.0%; Score 9; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAA 9
|||||
Db 7 GCTCTAGAA 15

RESULT 11

TA116E03P

LOCUS

DEFINITION
T. brucei sheared genomic DNA clone 116e03, forward sequence,
genomic survey sequence.

ACCESSION
AL462526

VERSION

KEYWORDS

SOURCE

ORGANISM

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source

1. .28
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="116e03"

BASE COUNT 7 a 5 c 8 g 8 t

ORIGIN

Query Match 60.0%; Score 9; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAATGAACG 15
|||||

Db 2 GAATGAACG 10

RESULT 12

AU257604

LOCUS

DEFINITION

AU257604 3'-directed mouse cDNA library Mus musculus cDNA clone

BE0011024 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Kato, K. and Matoba, R.

Generation of expressed sequence tags from mouse brain

Unpublished (2002)

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkatob@bs.aist-nara.ac.jp

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source

1. .30
/organism="Mus musculus"
/db_xref="taxon:10090"

```

/clone="BED0011024"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/notes="Vector: pGEM-T-easy"
BASE COUNT      13 a      6 c      4 g      7 t
ORIGIN

Query Match      60.0%; Score 9; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTCTAGAAT 10
Db      5 CTCTAGAAT 13

RESULT 13
AI032592/c
LOCUS
DEFINITION      ow73q08.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA
clone IMAGE:1652510 3' similar to TR:O15102 O15102 HYPOTHETICAL
40.0 KD PROTEIN. 1; mRNA sequence.
ACCESSION      AI032592
VERSION        AI032592.1 GI:3253718
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 31)
AUTHORS        NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL        Tumor Gene Index
COMMENT        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. Ef from Amerisham
High quality sequence stop: 1.
FEATURES       Location/Qualifiers
source         1..31
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:1652510"
               /clone_lib="Soares fetal liver spleen INFLS_S1"
               /sex="male"
               /dev_stage="20 week-post conception fetus"
               /lab_host="DH10B (ampicillin resistant)"
               /notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
               with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
               This is a subtracted version of the original Soares fetal
               liver spleen INFLS library. 1st strand cDNA was primed
               with a Pac I - oligo(dT) primer [5',
               AACTGGAAGTAATTAATAGATCTTTTTTTTTTTTTTTT 3'],
               double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Pac I and cloned into the Pac I
               and Eco RI sites of the modified pT7T3 vector. Library
               went through one round of normalization. Library
               constructed by Bento Soares and M.Fatima Bernaldo."
BASE COUNT      5 a      10 c      6 g      10 t
ORIGIN

Query Match      60.0%; Score 9; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TCTAGAATG 11
Db      28 TCTAGAATG 20

RESULT 14
BG339578
LOCUS
DEFINITION      34 bp mRNA linear EST-27-FEB-2001
602437433F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:455280 5',
mRNA sequence.
ACCESSION      BG339578
VERSION        BG339578.1 GI:13146016
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 34)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1256 row: a column: 09
High quality sequence stop: 34.
FEATURES       Location/Qualifiers
source         1..34
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:455280"
               /clone_lib="NIH MGC 46"
               /tissue_type="leiomyosarcoma cell line"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
               EcoRI; cDNA made by oligo-dT priming. Directionally cloned
               into EcoRI/XhoI sites using the following 5' adaptor:
               GGCACGAG(G). Size-selected >500bp for average insert size
               1.8kb. Library constructed by Ling Hong in the laboratory
               of Gerald M. Rubin (University of California, Berkeley)
               using ZAP-cDNA synthesis kit (Stratagene) and Superscript
               II RT (Life Technologies). Note: this is a NIH_MGC
               Library."
BASE COUNT      14 a      9 c      9 g      2 t
ORIGIN

Query Match      60.0%; Score 9; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGAATGAAC 14
Db      5 AGAATGAAC 13

RESULT 15
BG340055
LOCUS
DEFINITION      34 bp mRNA linear EST-27-FEB-2001
602438218F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4556092 5',
mRNA sequence.
ACCESSION      BG340055
VERSION        BG340055.1 GI:13146493
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 34)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLC1258 row: c column: 05
 High quality sequence stop: 34.

FEATURES

1. . . 34
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4556092"
 /clone_lib="NIH MGC 46"
 /tissue_type="leiomyosarcoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 14 a 9 c 9 g 2 t

ORIGIN

Query Match 60.0%; Score 9; DB 12; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAC 14
 |||||
 Db 5 AGAATGAC 13

Search completed: June 23, 2003, 10:10:27
 Job time : 774.52 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 658.446 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTTAGAATGAACG 15

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	100.0	21	1	PCT-US03-04088-539
C 2	15	100.0	21	1	PCT-US03-04088-539
C 3	15	100.0	21	1	PCT-US03-04088-543
C 4	15	100.0	21	1	PCT-US03-04088-547
C 5	15	100.0	21	1	PCT-US03-04088-551
C 6	15	100.0	21	1	PCT-US03-04088-555
C 7	15	100.0	21	1	PCT-US03-04088-559
C 8	15	100.0	21	1	PCT-US03-04088-521
C 9	15	100.0	26	6	US-09-721-456-598
C 10	15	100.0	26	9	US-10-325-810-598
C 11	15	100.0	26	9	US-10-325-810-598
C 12	15	100.0	26	9	US-10-359-935-23
C 13	15	100.0	30	10	US-10-330-872-5
C 14	14	93.3	23	9	US-10-330-872A-5
C 15	14	93.3	25	12	US-60-427-808-952738
C 16	14	93.3	25	13	US-60-469-545-13722
C 17	14	93.3	25	13	US-60-469-545-222991
C 18	13	86.7	18	6	US-09-721-456-543
C 19	13	86.7	18	9	US-10-325-810-543
C 20	13	86.7	21	1	PCT-US03-04088-538

21	13	86.7	21	1	PCT-US03-04088-542	Sequence 542, App
C 22	13	86.7	21	1	PCT-US03-04088-546	Sequence 546, App
C 23	13	86.7	21	1	PCT-US03-04088-550	Sequence 550, App
C 24	13	86.7	21	1	PCT-US03-04088-554	Sequence 554, App
C 25	13	86.7	21	1	PCT-US03-04088-558	Sequence 558, App
C 26	13	86.7	25	6	US-09-660-222-3845	Sequence 3845, App
C 27	13	86.7	25	6	US-09-660-222-3846	Sequence 3846, App
C 28	13	86.7	25	6	US-09-660-222-3854	Sequence 3854, App
C 29	13	86.7	25	9	US-10-098-263B-118949	Sequence 118949, App
C 30	13	86.7	25	9	US-10-355-577-173196	Sequence 173196, App
C 31	13	86.7	25	12	US-60-427-808-738286	Sequence 738286, App
C 32	13	86.7	25	12	US-60-427-836-267834	Sequence 267834, App
C 33	12	80.0	25	7	US-09-954-445A-17344	Sequence 17344, App
C 34	12	80.0	25	7	US-09-954-445A-17345	Sequence 17345, App
C 35	12	80.0	25	7	US-09-954-445A-17346	Sequence 17346, App
C 36	12	80.0	25	7	US-09-954-445A-17347	Sequence 17347, App
C 37	12	80.0	25	7	US-09-954-445A-17348	Sequence 17348, App
C 38	12	80.0	25	9	US-10-098-263B-64498	Sequence 64498, App
C 39	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 40	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 41	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 42	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 43	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 44	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App
C 45	12	80.0	25	9	US-10-355-577-70333	Sequence 70333, App

ALIGNMENTS

RESULT 1
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggan, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0% Score 15; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
|||:|||||
Db 19 GCTCTAGAAATGAACG 5

RESULT 2
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-543

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
|||:|||||
Db 1 GCUCUAGAUGAACG 15

RESULT 3
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 547
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxybasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
PCT-US03-04088-547

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
|||:|||||
Db 19 GCTCTAGAAATGAACG 5

RESULT 4
PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene


```

; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; PCT-US03-04088-551

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 1 GCUCUAGAAUGAACG 15

RESULT 5
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

```

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety
PCT-US03-04088-559

Query Match      100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 19 GCTCTAGAAATGAACG 5

RESULT 6
PCT-US03-04088-559
; Sequence 559, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(9)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559

Query Match      100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 1 GCUCUAGAAUGAAGC 15

RESULT 7
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-520

Query Match      100.0%; Score 15; DB 1; Length 23;
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 23 GCTCTAGAAATGAACG 9

RESULT 8
PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 100.0%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 21 GCTCTAGAAATGAACG 7

RESULT 9
US-09-721-456-598
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Haxley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-721-456-598

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
Db 5 GCTCTAGAAATGAACG 19

RESULT 10
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

```

; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598

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Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 11

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US-10-359-935-23
; Sequence 23, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; Funk, Junli
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23

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Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

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RESULT 12
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C

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; CURRENT APPLICATION NUMBER: US/10/330,872
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match      100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GCTCTAGAATGAACG 15

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match      100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAACG 15
Db      1 GCTCTAGAATGAACG 15

RESULT 14
US-10-310-188-36216/c
; Sequence 36216, Application US/10310168
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36216
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-36216

Query Match      93.3%; Score 14; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      14 GCTCTAGAATGAAC 1

RESULT 15
US-60-427-808-952738
; Sequence 952738, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 952738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-952738

Query Match      93.3%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAAC 14
Db      3 GCTCTAGAATGAAC 16

Search completed: June 23, 2003, 19:12:12
Job time : 658.446 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1258.09 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-10
Perfect score: 15
Sequence: 1 GCTTAGAATGAACG 15

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Gapop_60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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4	15	100.0	19	11	US-08-770-564A-9
5	15	100.0	25	16	US-09-250-336A-4
6	15	100.0	25	25	US-09-642-177-4
7	15	100.0	26	1	PCT-US96-14679-27
8	15	100.0	26	1	PCT-US96-14679A-27
9	15	100.0	26	1	PCT-US99-03302-4
10	15	100.0	26	1	PCT-US99-07533-4
11	15	100.0	26	1	PCT-US99-07533-4
12	15	100.0	26	6	US-08-272-102-23
13	15	100.0	26	7	US-08-387-524-19
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16	15	100.0	26	8	US-08-482-115A-23
17	15	100.0	26	9	US-08-520-550-19
18	15	100.0	26	9	US-08-521-634-41
19	15	100.0	26	10	US-08-660-678-23
20	15	100.0	26	13	US-08-911-312-23
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Sequence 9, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note= "oligo 21ab"
PCT-US97-23619-9
Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACG 15
Db 1 GCTCTAGAAATGAACG 15
RESULT 4
US-08-770-564A-9
Sequence 9, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-9
Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACG 15
Db 1 GCTCTAGAAATGAACG 15
RESULT 5
US-09-250-336A-4
Sequence 4, Application US/09250336A
GENERAL INFORMATION:
APPLICANT: STROVEL, Jeffrey W.
APPLICANT: STAMBERG, Judith
APPLICANT: ABRUZZO, Lynne V.
APPLICANT: HIGHSMITH, Edward
TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
FILE REFERENCE: 10460-4 (210460.0004)
CURRENT APPLICATION NUMBER: US/09/250,336A
CURRENT FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: US 60/074,793
PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: PCT/US99/03302
PRIOR FILING DATE: 1999-02-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4
Query Match 100.0%; Score 15; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAAATGAACG 15
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Db 4 GCTCTAGATGAACG 18

RESULT 6

US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: R3c, Primer
US-09-642-177-4

Query Match 100.0%; Score 15; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 4 GCTCTAGATGAACG 18

RESULT 7

PCT-US96-14679-27
; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779

; TELEFAX: (415)473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 8

PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415)473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 9

PCT-US99-03302-4

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/ Sequence 4, Application PC/TUS9903302
/ GENERAL INFORMATION:
/ APPLICANT: Strovel, Jeffrey W
/ APPLICANT: Stamborg, Judith
/ APPLICANT: Abruzzo, Lynne V
/ APPLICANT: Highsmith, Edward
/ TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
/ TITLE OF INVENTION: and Assessment of Disease Stage and Prognosis
/ FILE REFERENCE: 1489JS 60/074,793
/ CURRENT APPLICATION NUMBER: PCT/US99/03302
/ EARLIER FILING DATE: 1999-02-16
/ EARLIER APPLICATION NUMBER: 60/074,793
/ EARLIER FILING DATE: 1998-02-16
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 26
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: R3c,
/ OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 10
PCT-US99-07533-4
/ Sequence 4, Application PC/TUS9907533
/ GENERAL INFORMATION:
/ APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
/ TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
/ FILE REFERENCE: 07265/157W01
/ CURRENT APPLICATION NUMBER: PCT/US99/07533
/ EARLIER FILING DATE: 1999-04-06
/ EARLIER APPLICATION NUMBER: 60/080,783
/ EARLIER FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 26
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 11
PCT-US99-07533-4
/ Sequence 4, Application PC/TUS9907533A
/ GENERAL INFORMATION:
/ APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
/ TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
/ FILE REFERENCE: 07265/157W01
/ CURRENT APPLICATION NUMBER: PCT/US99/07533A
/ EARLIER FILING DATE: 1999-04-06
/ EARLIER APPLICATION NUMBER: 60/080,783
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/ EARLIER FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 26
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match          100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 12
US-08-272-102-23
/ Sequence 23, Application US/08272102
/ GENERAL INFORMATION:
/ APPLICANT: VILLEPONTEAU, Bryant
/ APPLICANT: FENG, Junli
/ APPLICANT: FUNK, Walter
/ APPLICANT: ANDREWS, William H.
/ TITLE OF INVENTION: HUMAN TELOMERASE
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Khourie and Crew
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/272.102
/ FILING DATE: 07-JUL-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William W
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 15389-000800
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-272-102-23

Query Match          100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 13
US-08-387-524-19
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; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millita Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-387-524-19

Query Match 100.0%; Score 15; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 14
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

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; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802A-24

Query Match 100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 15
US-08-472-802B-24
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994

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; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802B-24

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Query Match      100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAATGAACG 15
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Db       5 GCTCTAGAATGAACG 19

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Search completed: June 23, 2003, 16:08:21
Job time : 1258.16 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 120.538 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-10
Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0
Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published Applications_NA.*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	26	9	US-10-044-692-312
2	15	100.0	26	9	US-10-044-539-312
3	15	100.0	26	10	US-09-057-351-23
4	13	86.7	25	9	US-10-098-263B-118949
5	13	86.7	26	9	US-09-952-522B-19
6	13	86.7	28	10	US-09-844-006A-3
7	12	80.0	23	9	US-09-952-522B-17
8	12	80.0	23	9	US-09-952-522B-31
9	12	80.0	25	9	US-10-215-112-6862
10	12	80.0	25	9	US-10-098-263B-64498
11	12	80.0	26	9	US-10-011-366-16
12	11	73.3	21	9	US-09-997-868-13
13	11	73.3	22	10	US-09-765-873A-5
14	11	73.3	23	9	US-09-952-522B-9
15	11	73.3	24	9	US-10-245-813-2
16	11	73.3	25	9	US-10-098-263B-10750
17	11	73.3	25	9	US-10-098-263B-33532
18	11	73.3	25	9	US-10-098-263B-44593
19	11	73.3	25	9	US-10-098-263B-44594

c	20	11	73.3	25	9	US-10-098-263B-104702	Sequence 104702,
	21	11	73.3	26	9	US-10-118-495-11	Sequence 11, Appl
	22	11	73.3	26	9	US-10-118-495-13	Sequence 13, Appl
	23	11	73.3	27	10	US-09-784-508-8	Sequence 8, Appl
	24	11	73.3	29	9	US-10-162-223-2	Sequence 2, Appl
	25	11	73.3	31	10	US-09-905-983-40	Sequence 40, Appl
	26	11	73.3	33	9	US-09-848-616-12	Sequence 12, Appl
	27	11	73.3	33	9	US-09-964-895-7	Sequence 7, Appl
	28	11	73.3	33	9	US-09-964-895-15	Sequence 15, Appl
	29	11	73.3	34	10	US-09-784-508-10	Sequence 10, Appl
	30	11	73.3	36	9	US-10-166-183-14	Sequence 14, Appl
c	31	11	73.3	36	9	US-10-127-816-18	Sequence 18, Appl
	32	11	73.3	36	10	US-09-784-508-11	Sequence 11, Appl
	33	10	66.7	21	8	US-08-913-322-3	Sequence 3, Appl
	34	10	66.7	21	10	US-09-767-479-15	Sequence 15, Appl
	35	10	66.7	22	9	US-09-981-648-11	Sequence 11, Appl
c	36	10	66.7	23	9	US-09-989-708-2	Sequence 2, Appl
	37	10	66.7	23	9	US-10-071-485-49	Sequence 49, Appl
	38	10	66.7	24	9	US-09-911-176B-24	Sequence 24, Appl
c	39	10	66.7	24	9	US-10-180-762-24	Sequence 24, Appl
	40	10	66.7	24	9	US-10-241-258-24	Sequence 24, Appl
c	41	10	66.7	25	9	US-10-098-263B-1399	Sequence 1399, Ap
c	42	10	66.7	25	9	US-10-098-263B-5826	Sequence 5826, Ap
c	43	10	66.7	25	9	US-10-098-263B-8894	Sequence 8894, Ap
c	44	10	66.7	25	9	US-10-098-263B-60549	Sequence 60549, A
c	45	10	66.7	25	9	US-10-098-263B-63103	Sequence 63103, A

ALIGNMENTS

RESULT 1

US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/044,692

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

```

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312

Query Match      100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
Db      5 GCTCTAGATGAACG 19

RESULT 2
US-10-044-539-312
; Sequence 312, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match      100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
Db      5 GCTCTAGATGAACG 19

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
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; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match      100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
Db      5 GCTCTAGATGAACG 19

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
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100

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; SOFTWARE: FACILITY ver. 2.0.1
; SEQ ID NO 17
; LENGTH: 23

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
; OTHER INFORMATION: forward primer
US-09-952-522B-17

Query Match      80.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAATGA 12
      |||||
Db      1 GCTCTAGAATGA 12

RESULT 8
US-09-952-522B-31
; Sequence 31, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSB-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
; OTHER INFORMATION: forward primer
US-09-952-522B-31

Query Match      80.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAATGA 12
      |||||
Db      1 GCTCTAGAATGA 12

RESULT 9
US-10-215-112-6862/c
; Sequence 6862, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6862
; LENGTH: 25

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-10-215-112-6862

Query Match      80.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAATGA 12
      |||||
Db      15 GCTCTAGAATGA 4

RESULT 10
US-10-098-263B-64498/c
; Sequence 6498, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64498
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64498

Query Match      80.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TCTAGAATGAAC 14
      |||||
Db      23 TCTAGAATGAAC 12

RESULT 11
US-10-011-366-16
; Sequence 16, Application US/10011366
; Publication No. US20030054493A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Kink, John A.
; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
DISEASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/011,366
; APPLICATION NUMBER: US/10/011,366
; FILING DATE: 16-NO. US20030054493A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,310

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;; FILING DATE: 23-OCT-1997
;; APPLICATION NUMBER: US 08/329,154
;; FILING DATE: 24-OCT-1994
;; APPLICATION NUMBER: US 08/161,907
;; FILING DATE: 02-DEC-1993
;; APPLICATION NUMBER: US 07/985,321
;; FILING DATE: 04-DEC-1992
;; APPLICATION NUMBER: US 07/429,791
;; FILING DATE: 31-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: OPHD-01121
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16

Query Match 80.0%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
|||
DB 1 GCTCTAGATGA 12

RESULT 12
US-09-997-868-13/c
;; Sequence 13, Application US/09997868
;; Publication No. US20030031654A1
;; GENERAL INFORMATION:
;; APPLICANT: Gorman, Cornelia M.,
;; TITLE OF INVENTION: Polihormone Convertase Transformed Cells and
;; Polypeptide Synthesis
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/997,868
;; FILING DATE: 12-Mar-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/887265
;; FILING DATE: 22-MAY-1992
;; APPLICATION NUMBER: 07/803631
;; FILING DATE: 06-DEC-1992
;; APPLICATION NUMBER: PCT/US92/10621
;; FILING DATE: 04-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P0748P3
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match 73.3%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||
DB 11 GCTCTAGATG 11

RESULT 13
US-09-765-873A-5
;; Sequence 5, Application US/09765873A
;; Patent No. US20010053847A1
;; GENERAL INFORMATION:
;; APPLICANT: Tang, Xiao-Song
;; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
;; FILE REFERENCE: BC1009 US CIP
;; CURRENT APPLICATION NUMBER: US/09/765,873A
;; CURRENT FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: US 09/627,216
;; PRIOR FILING DATE: 2000-07-27
;; PRIOR APPLICATION NUMBER: US 60/147,719
;; PRIOR FILING DATE: 1999-08-06
;; NUMBER OF SEQ ID NOS: 38
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 5
;; LENGTH: 22
;; TYPE: DNA
;; ORGANISM: primer
;; US-09-765-873A-5

Query Match 73.3%; Score 11; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||
DB 3 GCTCTAGATG 13

RESULT 14
US-09-952-522B-9
;; Sequence 9, Application US/09952522B
;; Publication No. US20030082152A1
;; GENERAL INFORMATION:
;; APPLICANT: Katz, Adam J.
;; APPLICANT: Lull, Ramon
;; APPLICANT: Putrell, J. William
;; APPLICANT: Hedrick, Marc H.
;; APPLICANT: Benhaim, Prosper
;; APPLICANT: Lorenz, Hermann Peter
;; APPLICANT: Zhu, Min
;; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
;; FILE REFERENCE: 30448.77US11
;; CURRENT APPLICATION NUMBER: US/09/952,522B
;; CURRENT FILING DATE: 2001-09-10
;; PRIOR APPLICATION NUMBER: PCT/US00/06232
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: 60/123,711
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/162,462
;; PRIOR FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: osteocalcin forward primer
US-09-952-522B-9

Query Match 73.3%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
| | | | | | | | | |
Db 1 GCTCTAGATG 11

RESULT 15
US-10-245-813-2
; Sequence 2, Application US/10245813
; Publication No. US2003060443A1
; GENERAL INFORMATION:
; APPLICANT: Gyun Min Lee
; APPLICANT: No. US2003060443A1Soo Kim
; TITLE OF INVENTION: INHIBITION OF APOPTOSIS BY THE
; TITLE OF INVENTION: EXPRESSION OF ANTISENSE RNA OF CASPASE-2
; FILE REFERENCE: 118.19-US-01
; CURRENT APPLICATION NUMBER: US/10/245,813
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 2001-57353
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: casp3L primer
US-10-245-813-2

Query Match 73.3%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
| | | | | | | | | |
Db 1 GCTCTAGATG 11

Search completed: June 23, 2003, 20:01:32
Job time : 120.538 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 23.4861 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-10
Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
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6: /cgn2_6/prodata/2/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	2	US-08-770-565-10
2	15	100.0	19	2	US-08-770-565-9
3	15	100.0	26	1	US-08-330-123A-23
4	15	100.0	26	1	US-08-482-115B-23
5	15	100.0	26	2	US-08-660-678A-23
6	15	100.0	26	2	US-08-710-249-26
7	15	100.0	26	2	US-08-485-778-19
8	15	100.0	26	2	US-08-472-802C-24
9	15	100.0	26	3	US-08-520-550A-19
10	15	100.0	26	3	US-08-998-443-23
11	15	100.0	26	4	US-08-974-549A-598
12	15	100.0	26	4	US-09-060-523-23
13	15	100.0	26	4	US-09-220-157A-26
14	15	100.0	26	4	US-09-286-959B-4
15	15	100.0	26	4	US-09-580-517-23
16	15	100.0	27	2	US-08-770-565-26
17	15	100.0	30	2	US-08-770-565-8
18	14	93.3	27	3	US-08-630-172-24
19	14	93.3	27	3	US-09-375-419-24
20	14	93.3	30	2	US-08-833-377-6
21	13	86.7	18	4	US-08-974-549A-543
22	12	80.0	26	1	US-08-480-604A-16
23	12	80.0	26	2	US-08-405-496A-16
24	12	80.0	26	4	US-08-915-136-16
25	12	80.0	26	4	US-08-957-310-16
26	12	80.0	30	1	US-08-349-006-3
27	12	80.0	30	5	PCT-US94-02107-3

28	12	80.0	33	3	US-08-630-172-22	Sequence 22, Appl
29	12	80.0	33	4	US-09-375-419-22	Sequence 22, Appl
30	11	73.3	11	2	US-08-770-565-11	Sequence 11, Appl
C 31	11	73.3	21	4	US-08-026-143B-13	Sequence 13, Appl
C 32	11	73.3	21	5	PCT-US92-10621-13	Sequence 13, Appl
C 33	11	73.3	21	5	PCT-US94-02233-13	Sequence 13, Appl
34	11	73.3	22	4	US-09-627-216A-5	Sequence 5, Appl
35	11	73.3	23	3	US-08-973-068-46	Sequence 46, Appl
36	11	73.3	26	4	US-09-153-310-4	Sequence 4, Appl
37	11	73.3	30	2	US-08-995-927-7	Sequence 7, Appl
38	11	73.3	30	4	US-09-349-627-5	Sequence 5, Appl
39	11	73.3	30	4	US-09-582-096-7	Sequence 7, Appl
40	11	73.3	37	1	US-08-591-492-17	Sequence 17, Appl
41	11	73.3	37	3	US-08-815-190A-3	Sequence 3, Appl
42	11	73.3	39	4	US-09-091-305-3	Sequence 3, Appl
43	11	73.3	40	1	US-08-395-800A-12	Sequence 12, Appl
C 44	11	73.3	46	1	US-08-399-696-14	Sequence 14, Appl
C 45	10	66.7	15	2	US-08-624-601-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-10
; Sequence 10, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-10

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15

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STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels

QY 1 GCTCTAGATGAACG 15
    |||||
Db 5 GCTCTAGATGAACG 19

RESULT 4
US-08-482-115B-23
; Sequence 23, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Vallepointeau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123

```

;; FILING DATE: 27-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015389-000830US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 5
US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-660-678A-23

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 6
US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 7
US-08-485-778-19
; Sequence 19, Application US/08485778

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; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-485-778-19

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 8
US-08-472-802C-24
; Sequence 24, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802C-24

Query Match 100.0%; Score 15; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 9
US-08-520-550A-19
; Sequence 19, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-19

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 10
US-08-998-443-23
Sequence 23, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 100.0%; Score 15; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 11
US-08-974-549A-598
Sequence 598, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA: WO PCT/US97/17618
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 12
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-060-523-23

Query Match 100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 13
US-09-220-157A-26
Sequence 26, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,157A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-220-157A-26

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 14
US-09-286-959B-4
; Sequence 4, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-286-959B-4

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 15
US-09-580-517-23
; Sequence 23, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,517
; FILING DATE: 25-May-2000
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,123
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match      100.0%; Score 15; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

Search completed: June 23, 2003, 10:17:07
Job time : 23.4861 secs
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 99.6813 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	19	AAV41177 RNA component of h
2	15	100.0	19	19	AAV41176 RNA component of h
3	15	100.0	25	20	AAZ08704 Human telomerase R
4	15	100.0	26	17	AAT10304 RNA component of h
5	15	100.0	26	17	AAT10299 RNA component of h
6	15	100.0	26	17	AAT11044 Primer for product
7	15	100.0	26	18	AAT58811 Human telomerase P
8	15	100.0	26	19	AAV19489 Human htr gene R
9	15	100.0	26	19	AAV17033 Telomerase PCR pri

10	15	100.0	26	20	AAZ08704	Human telomerase R
11	15	100.0	26	20	AAZ07402	Human telomerase R
12	15	100.0	26	20	AAZ01542	PCR primer for Hum
13	15	100.0	26	21	AAZ08250	Human telomerase R
14	15	100.0	26	24	ABK48024	Human telomerase-a
15	15	100.0	26	24	AAZ02426	Human telomerase (
16	15	100.0	27	19	AAV41193	RNA component of h
17	15	100.0	27	24	AAZ05497	Human telomerase R
18	15	100.0	30	19	AAZ03649	Antisense oligonuc
19	15	100.0	30	19	AAV41175	RNA component of h
20	15	100.0	30	20	AAZ023631	Human clone 28-1 t
21	15	100.0	30	22	AAZ03476	Antisense oligonuc
22	15	100.0	30	23	AAZ015928	Human telomerase p
23	15	100.0	30	24	AAZ01517	Oligonucleotide us
24	14	93.3	27	18	AAZ07049	Sense primer for h
25	13	86.7	23	23	AAZ015930	Human telomerase p
26	13	86.7	28	24	ABA04366	CRT C-domain-green
27	13	86.7	32	21	AAZ06113	Human GPCR TDAG8(I
28	12	80.0	17	22	AAZ057369	Murine Cdc25A intr
29	12	80.0	26	17	AAZ029258	C. difficile toxin
30	12	80.0	26	19	AAZ030567	Clostridium diffic
31	12	80.0	26	21	ABK09963	Novel recombinant
32	12	80.0	30	15	AAZ071630	HCMV IE-exon-4 sub
33	12	80.0	33	18	AAZ07047	Sense primer for h
34	12	80.0	39	22	AAZ081502	Novel human G prot
35	12	80.0	39	22	AAZ087602	RNA associated wit
36	11	73.3	11	19	AAZ01178	RNA component of h
37	11	73.3	11	23	AAZ015929	Human telomerase p
38	11	73.3	19	22	AAZ043421	IS3 reverse prime
39	11	73.3	21	14	AAZ043258	Sequence encoding
40	11	73.3	21	14	AAZ043257	Sequence encoding
41	11	73.3	21	15	AAZ071457	Rx 2.4 prtelaxin
42	11	73.3	22	24	AAZ033073	Phenylalanine ammo
43	11	73.3	22	24	AAZ026921	Rhodospiridium tor
44	11	73.3	23	18	AAZ049421	Banana bunchy top
45	11	73.3	24	19	AAZ043976	C. sativa chloropl

ALIGNMENTS

RESULT 1
AAV41177
ID AAV41177 standard; DNA; 15 BP.
XX
AC AAV41177;
XX
DT 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) antisense oligo 21ab3.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; htr;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX Synthetic.
OS Homo sapiens.
XX
PN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
DR

XX New polynucleotide(s) anti:sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 XX Claim 11; Page 65; 80pp; English.
 XX
 CC Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridise to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridise to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting the
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX
 SQ Sequence 19 BP; 5 A; 3 C; 7 G; 4 T; 0 other;
 Query Match 100.0%; Score 15; DB 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACG 15
 DB 1 GCTCTAGATGAACG 15
 RESULT 3
 AAZ08704
 ID AAZ08704 standard; DNA; 25 BP.
 XX
 AC AAZ08704;
 XX
 DT 20-OCT-1999 (first entry)
 XX
 DE Human telomerase RNA template PCR primer R3C.
 XX
 KW Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
 KW telomeric repeat amplification protocol; detection; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9941406-A1.
 XX
 PD 19-AUG-1999.
 XX
 PF 16-FEB-1999; 99WO-US03302.
 XX
 PR 16-FEB-1998; 98US-0074793.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 PI Abruzzo LV, Highsmith E, Stamborg J, Strovel JW;
 XX
 DR WPI; 1999-508655/42.
 XX
 PT Detecting telomerase activity in non-cellular body fluid using a
 PT modified telomeric repeat amplification protocol
 XX
 PS Disclosure; Page 16; 32pp; English.

XX New polynucleotide(s) anti:sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 XX Claim 11; Page 65; 80pp; English.
 XX
 CC Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridise to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridise to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting the
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX
 SQ Sequence 15 BP; 5 A; 3 C; 4 G; 3 T; 0 other;
 Query Match 100.0%; Score 15; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACG 15
 DB 1 GCTCTAGATGAACG 15
 RESULT 2
 AAV41176
 ID AAV41176 standard; DNA; 19 BP.
 XX
 AC AAV41176;
 XX
 DT 08-OCT-1998 (first entry)
 XX
 DE RNA component of human telomerase (hTR) antisense oligo 21ab.
 XX
 KW RNA component; human telomerase; antisense oligonucleotide; infection;
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KW contraception; sterilisation; immuno-suppression; therapeutic; hTR;
 KW immune system down-regulation; anti-inflammatory therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9828442-A1.
 XX
 PD 02-JUL-1998.
 XX
 PF 19-DEC-1997; 97WO-US23619.
 XX
 PR 20-DEC-1996; 96US-0770565.
 PR 20-DEC-1996; 96US-0770564.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
 XX
 DR WPI; 1998-377670/32.
 XX

XX A method has been developed for detecting telomerase activity in a
 CC non-cellular portion of body fluid from a cancer patient using a
 CC modified telomeric repeat amplification protocol (TRAP). A method for
 CC detecting cancer comprises: (a) removing the cellular portion of a body
 CC fluid specimen from the patient; (b) preparing a protein extract from
 CC the body fluid remainder; (c) assaying the extract for the presence and
 CC quantity of telomerase RNA or telomerase activity; and (d) comparing the
 CC results with normal levels, to determine the presence of cancer. The
 CC methods are used in cancer diagnosis and prognosis, and also to monitor
 CC cancer therapy effectiveness. Unlike prior art telomerase activity
 CC assays in cancer patients, the method allows noninvasive sample
 CC collection. The methods are also more reliable and less tumour specific
 CC than other methods which detect circulating tumour markers. The present
 CC sequence represents a human telomerase RNA template PCR primer used in
 CC the exemplification of the present invention.

XX Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTAACG 15

DB 4 GCTCTAGAGTAACG 18

RESULT 4

AAT10304
 ID AAT10304 standard; DNA; 26 BP.

AC AAT10304;

XX 10-SEP-1996 (first entry)

DE RNA component of human telomerase nested PCR primer R3c.

XX RNA component; human; telomerase; polymerase chain reaction;
 KW recombinant production; synthesis; mutant; detection; mammalian;
 KW identification; modulating agent; neoplastic condition;
 KW transcriptional regulatory sequence; gene therapy; disease;
 KW PCR primer; ss.

XX Synthetic.

OS WO9601835-A1.

PN 25-JAN-1996.

XX 06-JUL-1995; 95WO-US08530.

PR 07-JUN-1995; 95US-0482115.

PR 07-JUL-1994; 94US-0272102.

PR 27-OCT-1994; 94US-0330123.

PR 07-JUN-1995; 95US-0472802.

XX (GERO-) GERON CORP.

PA Andrews WH, Feng J, Funk W, Villeponteau B;

PI WPI; 1996-097581/10.

DR RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents

XX Example 10; Page 82; 114pp; English.

PS The present sequence, a nested PCR primer for the RNA component
 CC of human telomerase (RCHT), was used in a 5' RACE procedure. The
 CC RCHT can be used in the recombinant prodn. of an active telomerase
 CC mol., capable of adding sequences to chromosomal DNA telomeres, and
 CC in the synthesis of mutant sequences for the detection of mutant

CC mammalian telomerase RNA component polynucleotides. The RCHT may
 CC also be used in the identification of telomerase modulating agents,
 CC and in the detection of telomerase related, or neoplastic
 CC conditions in a patient. Polynucleotides of at least 25
 CC consecutive nucleotides identical, or complementary to the RCHT
 CC sequence linked to heterologous transcriptional regulatory
 CC sequences, can be used for the gene therapy of human diseases.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTAACG 15

DB 5 GCTCTAGAGTAACG 19

RESULT 5

AAT10299

ID AAT10299 standard; DNA; 26 BP.

XX AAT10299;

XX 09-SEP-1996 (first entry)

DE RNA component of human telomerase antisense plasmid PCR primer R3C.

XX RNA component; human; telomerase; lung fibroblast; cell line WI-38;
 KW recombinant production; synthesis; mutant; detection; mammalian;
 KW identification; modulating agent; neoplastic condition;
 KW transcriptional regulatory sequence; gene therapy; disease;
 KW polymerase chain reaction; antisense plasmid; PCR primer; ss.

XX Synthetic.

OS WO9601835-A1.

PN 25-JAN-1996.

XX 06-JUL-1995; 95WO-US08530.

PR 07-JUN-1995; 95US-0482115.

PR 07-JUL-1994; 94US-0272102.

PR 27-OCT-1994; 94US-0330123.

PR 07-JUN-1995; 95US-0472802.

XX (GERO-) GERON CORP.

PA Andrews WH, Feng J, Funk W, Villeponteau B;

PI WPI; 1996-097581/10.

DR RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents

XX Example 8; Page 80; 114pp; English.

PS The present sequence is a PCR primer for a RNA component of human
 CC telomerase (RCHT), antisense plasmid. RCHT was derived from a
 CC genomic DNA library obtd. from the human lung fibroblast cell line
 CC WI-38. The RCHT can be used in the recombinant prodn. of an active
 CC telomerase mol., capable of adding sequences to chromosomal DNA
 CC telomeres, and in the synthesis of mutant sequences for the
 CC detection of mutant mammalian telomerase RNA component
 CC polynucleotides. The RCHT may also be used in the identification
 CC of telomerase modulating agents, and in the detection of
 CC telomerase related, or neoplastic conditions in a patient.
 CC Polynucleotides of at least 25 consecutive nucleotides identical,
 CC or complementary to the RCHT sequence linked to heterologous
 CC transcriptional regulatory sequences, can be used for the gene
 CC therapy of human diseases.

SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 17; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3; 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 QY 1 GCTCTAGATGAACG 15
 Db 5 GCTCTAGATGAACG 19

RESULT 6
 AAT11044
 ID AAT11044 standard; DNA; 26 BP.
 XX
 AC AAT11044;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Primer for production of telomerase antisense oligonucleotide.
 XX
 KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KW plasmid; probe; primer; ribozyme; ss.
 XX
 OS Synthetic.
 XX
 PN WO9601614-A2.
 XX
 PD 25-JAN-1996.
 XX
 PF 07-JUL-1995; 95WO-US08620.
 XX
 PR 07-JUN-1995; 95US-0485778.
 PR 07-JUL-1994; 94US-0272102.
 PR 27-OCT-1994; 94US-0330123.
 PR 13-FEB-1995; 95US-0387524.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (GERO-) GERON CORP.
 XX
 PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
 PI Marhuenda MA, Villeponteau B;
 XX
 DR WPI; 1996-097428/10.
 XX
 XX RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 PT
 XX Example 8; Page 53; 85pp; English.
 XX
 CC The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the
 CC telomerase gene (also claimed) can be used for study of telomere
 CC regulation in vivo, and the role it plays in immortalisation.
 CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
 CC antisense oligonucleotides which were then used to produce antisense
 CC expression plasmids. AAT11040 was used alongside both AAT11043 and
 CC AAT11044 to produce two different antisense molecules.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 17; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 7
 AAT58811
 ID AAT58811 standard; DNA; 26 BP.
 XX
 AC AAT58811;
 XX
 DT 20-NOV-1997 (first entry)
 XX
 DE Human telomerase PCR 3'-primer R3C.
 XX
 KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
 KW protozoa; tumour; antibody; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640868-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09517.
 XX
 PR 07-JUN-1995; 95US-0478352.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Autexier C, Greider C;
 XX
 DR WPI; 1997-099928/09.
 XX
 PT DNA encoding essential RNA components of human telomerase - also
 PT truncated or recombinant telomerase, useful for diagnosis and
 PT treatment of cancer and infection by eukaryotic parasites
 XX
 XX Example 5; Page 32; 48pp; English.
 XX
 CC The present sequence represents PCR 3'-primer R3C used for
 CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
 CC hybridisation assays to detect or quantify telomerase activity in cells,
 CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
 CC (yeast and protozoa) or tumours. It is also useful as primers for
 CC amplification assays. The truncated or recombinant vertebrate telomerase
 CC is used therapeutically to increase telomerase activity (also as
 CC reagents in the screening assay) while the RNA or other inhibitors such
 CC as antisense molecules, are used to reduce such activity. Typical
 CC applications are initiation/restoration of activity to cause senescence
 CC or to prevent immortalisation of cells in tumours or parasites. The DNA
 CC is also used to produce recombinant telomerase, which can then be used
 CC conventionally to raise antibodies for diagnostic detection of
 CC telomerase. Detecting telomerase allows early diagnosis of tumour or
 CC infection, before clinical signs manifest. Telomerase inhibitors
 CC directed against e.g. Trypanosoma should cause fewer side effects than
 CC drugs currently used to treat such infections. The DNA encodes those
 CC parts of hTR RNA essential for activity but are significantly shorter
 CC than the endogenous RNA component.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 18; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACG 15
 Db 5 GCTCTAGATGAACG 19

RESULT 8
 AAV19489
 ID AAV19489 standard; DNA; 26 BP.


```

XX AAV19489;
AC
XX
XX 28-AUG-1998 (first entry)
XX
XX Human hTR gene RT-PCR primer R3c.
DE
XX
XX hTR gene; TPC2; TPC3; telomere length; telomerase; human; cancer;
KW Gene therapy; diagnosis; PCR; primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9811204-A1.
FN
XX
XX 19-MAR-1998.
PD
XX
XX 13-SEP-1996; 96WO-US14679.
PF
XX
XX 13-SEP-1996; 96WO-US14679.
PR
XX (GERO-) GERON CORP.
PA
XX Adams RR, Andrews WH, Feng J, Villeponteau B;
PI
XX WPI; 1998-207373/18.
DR
XX
XX Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
PT telomerase activity
PT
XX Disclosure; Page 49; 86pp; English.
XX
XX Primers R3c and F3b (see AAV19488) were designed for the PCR
CC amplification of the human telomerase hTR gene (see AAV19481). hTR
CC mRNA levels were showed to correlate with telomerase activity
CC levels in a variety of mortal and immortal cell lines. Methods of
CC the invention allow detection and quantitation of TPC2 (see
CC AAV19479), TPC3 (see AAV19480) and/or TPC2 gene products and can be
CC used to detect immortal cells, especially telomerase positive
CC cancer cells.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 15; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 9
AAV17033
ID AAV17033 standard; DNA; 26 BP.
XX
XX AAV17033;
AC
XX
XX 13-AUG-1998 (first entry)
DE
XX Telomerase PCR primer R3c.
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
KW PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX GB2317891-A.
PN
XX
XX 08-APR-1998.
XX

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PF 01-OCT-1997; 97GB-0020890.
XX
XX 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
PI Morin GB, Nakamura T, Harley CB;
XX
XX WPI; 1998-171633/16.
DR
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of
PT cell proliferation conditions especially cancer and ageing
XX
XX Example 2; Page 218; 387pp; English.
XX
XX The present sequence represents a PCR primer from the present invention
CC which describes human telomerase reverse transcriptase (hTERT). The
CC present invention also describes the following methods: (A) determining
CC whether a test compound is a modulator of hTERT, by detecting the change
CC in hTERT recombinant protein or polynucleotide, on administration of the
CC compound; (B) preparation of recombinant telomerase by contacting a
CC protein preparation of hTERT with a telomerase RNA component; (C)
CC detection of the hTERT RNA or protein in a sample by binding a relevant
CC probe to the sample and detecting the complex formed or in the case of
CC RNA detection, amplifying the product and correlating the presence of
CC complex or amplification product with presence of hTERT in the sample;
CC and (D) increasing the proliferation of a vertebrate cell by increasing
CC hTERT expression; and (E) the use of an agent that causes an increase in
CC cell vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be
CC used to treat conditions that are associated with high telomerase
CC activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 15; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19

RESULT 10
AAV90788
ID AAV90788 standard; DNA; 26 BP.
XX
XX AAV90788;
AC
XX
XX 13-JAN-2000 (first entry)
DT
XX Human telomerase RNA specific PCR primer-2.
DE
XX
XX PCR primer; human telomerase RNA; hTR; amplify; human staufen cDNA;
KW hTERT; synthesised; random hexamer primer;
KW Superscript II reverse transcriptase; ss.
XX
XX Synthetic.
OS Homo sapiens.

```

XX WO9951255-A1.
 XX PD 14-OCT-1999.
 XX PF 06-APR-1999; 99WO-US07533.
 XX PR 06-APR-1998; 98US-0080783.
 XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PI Greider CW, Le S;
 XX WP 1999-620168/53.
 XX Human staufen polypeptide useful in methods for identifying telomerase
 XX inhibitors -
 XX PS Disclosure; Page 15; 50pp; English.
 XX CC The present sequence is a PCR primer specific to human telomerase
 XX RNA (hTR). It is used to amplify human staufen (hStau) cDNA synthesised
 XX CC using random hexamer primers and Superscript II reverse transcriptase.
 XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATGAACG 15
 Db 5 GCTCTAGAATGAACG 19
 RESULT 11
 AAX77402
 ID AAX77402 standard; DNA; 26 BP.
 XX AC AAX77402;
 XX DT 05-AUG-1999 (first entry)
 XX DE Human telomerase RNA PCR primer TE-hTR3.1.
 XX KW Telomerase; human; diagnosis; bladder cancer; detection; urine;
 XX KW PCR primer; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN EP926245-A2.
 XX PD 30-JUN-1999.
 XX PF 21-DEC-1998; 98EP-0124326.
 XX PR 22-DEC-1997; 97DE-1057300.
 XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX PI Emrich T;
 XX WP 1999-349242/30.
 XX Detecting telomerase RNA in urine - useful for diagnosis of bladder
 XX cancer
 XX PS Claim 6; Page 10; 13pp; German.
 XX CC This invention describes a novel method for diagnosing bladder cancer,
 XX CC which comprises detecting telomerase RNA in a urine sample. The method
 XX CC of the invention has greater sensitivity and reliability than assays for

CC telomerase activity (cf. WO 9735871). This sequence represents a primer
 CC used in the method of the invention.
 XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATGAACG 15
 Db 5 GCTCTAGAATGAACG 19
 RESULT 12
 AAX01542
 ID AAX01542 standard; DNA; 26 BP.
 XX AC AAX01542;
 XX DT 29-APR-1999 (first entry)
 XX DE PCR primer for Human TPC3 gene.
 XX KW TPC2; TPC3; human; telomere length regulation; cancer; pregnancy;
 XX KW fertility; diagnosis; therapy; PCR primer; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN US5858777-A.
 XX PD 12-JAN-1999.
 XX PF 13-SEP-1996; 96US-0710249.
 XX PR 08-SEP-1995; 95US-0003492.
 XX PR 05-JAN-1996; 96US-0583808.
 XX PR 13-SEP-1996; 96US-0710249.
 XX PA (GERO-) GERON CORP.
 XX PI Adams RR, Andrews WH, Feng J, Villeponteau B;
 XX WP 1999-152104/13.
 XX DNA encoding proteins TPC2 and TPC3 - useful for regulating telomere
 XX length or modulating telomerase activity
 XX PS Example; Column 38; 59pp; English.
 XX CC This sequence represents a PCR primer for DNA encoding the human TPC3
 XX CC protein, which is contained within the recombinant mammalian host cell of
 XX CC the invention. The invention provides methods and reagents for regulating
 XX CC telomere length and modulating telomerase activity in mammalian cells as
 XX CC well as for detecting, diagnosing, and treating related diseases and
 XX CC conditions such as cancer, pregnancy, or fertility in humans and other
 XX CC mammals.
 XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 15; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATGAACG 15
 Db 5 GCTCTAGAATGAACG 19
 RESULT 13
 AAA88250
 ID AAA88250 standard; DNA; 26 BP.

XX AAA88250;
 AC 15-DEC-2000 (first entry)
 DT Human telomerase RNA reverse transcriptase PCR primer #2.
 DE Human; telomerase; hTR; reverse transcriptase; RT-PCR; PCR primer;
 KW detection; cancer; micrometastasis; diagnosis; ss.
 XX Homo sapiens.
 OS
 XX WO200046601-A1.
 PN 10-AUG-2000.
 PD
 XX 01-FEB-2000; 2000WO-1B00100.
 XX 02-FEB-1999; 99GB-0002302.
 XX (LARS/) LARSEN F.
 PA (SKAA/) SKAANSENG M.
 XX Larsen F, Skaanseng M;
 XX WPI; 2000-491281/43.
 DR
 XX Detecting telomerase activity in samples, useful for diagnosis of
 PT cancer and micrometastasis, comprises treating sample with solid phase,
 PT removing solid phase and treating to elute bound telomerase -
 XX Example 11; Page 38; 68pp; English.
 PS
 XX The present invention describes a method (I) for detecting telomerase
 CC activity in a sample. The method comprises treating the sample with a
 CC solid phase to bind telomerase, separating the solid phase from the
 CC sample to form a test sample which may be treated to elute bound
 CC telomerase and assaying the sample for telomerase activity. Also
 CC described are: (1) a kit (II) for detecting telomerase activity,
 CC comprising a solid phase and one or more components for assaying
 CC telomerase activity; and (2) a component (III) of an assay system for
 CC detecting telomerase activity, comprising a solid phase for binding
 CC telomerase on which is present a substrate for telomerase elongation.
 CC (I) is useful for cancer diagnosis or prognosis and detection of
 CC micrometastasis as detection of telomerase activity is indicative of
 CC cancer or micrometastasis. The solid phase used in (I) is useful for
 CC separating telomerase from a sample and therefore for detecting
 CC telomerase activity. (II) is useful for detection of cancer cells and
 CC may also comprises means for assaying an mRNA diagnostic for cancer.
 CC The present sequence represents a reverse transcriptase (RT) PCR primer
 CC for human telomerase RNA, which is used in an example from the present
 CC invention.
 XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 SQ
 Query Match 100.0%; Score 15; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTCTAGATGAACG 15
 Db 5 GCTCTAGATGAACG 19
 RESULT 14
 ABK48024
 ID ABK48024 standard; DNA; 26 BP.
 XX
 AC ABK48024;
 XX
 XX 18-JUN-2002 (first entry)
 DT Human telomerase-associated RNA template (hTR), PCR primer hTR2.
 DE

XX Human; telomerase-associated RNA template; hTR; endometrial;
 KW malignancy; cancer; breast; ovarian; head and neck; lung; cervical;
 KW colorectal; gastric; liver; pancreatic; bladder; prostate;
 KW brain; kidney; oesophagus; melanoma; sarcoma; premalignancy;
 KW carcinoma in-situ; cervical dysplasia; bronchial dysplasia;
 KW cervical intraepithelial neoplasia; atypical hyperplasia;
 KW colorectal adenoma; atypical endometrial hyperplasia; tumour;
 KW Barrett's oesophagus; telomerase-directed therapy; primer; ss.
 XX Homo sapiens.
 OS
 XX WO200218652-A2.
 PN 07-MAR-2002.
 PD
 XX 28-AUG-2001; 2001WO-US26749.
 XX 31-AUG-2000; 2000US-0653573.
 XX (ONCO-) ONCOMEDX INC.
 PA Kopreski MS, Gocke CD;
 XX WPI; 2002-269532/31.
 DR
 XX Detecting human telomerase RNA template RNA or human telomerase reverse
 PT transcriptase protein RNA in bodily fluid, useful as marker for
 PT diagnosing, monitoring or treating cancer, carcinoma in situ or
 PT premalignancy -
 XX Example 1; Page 14; 30pp; English.
 PS
 XX The invention relates to detecting human telomerase RNA template (hTR)
 CC RNA or human telomerase reverse transcriptase protein RNA (hRTP) RNA (I)
 CC in a bodily fluid, comprising amplifying RNA extracted from plasma or
 CC serum sample, or its corresponding cDNA comprising (I), using primers or
 CC probes that target (I) or cDNA and detecting qualitatively or
 CC quantitatively amplified product of (I) or cDNA product. The method is
 CC useful for detecting (I) in a bodily fluid, which is useful for
 CC identifying a human having (I) expressing cells or tissue which
 CC include a malignancy preferably a cancer of breast, ovarian, head and
 CC neck, lung, cervical, colorectal, gastric, liver, pancreatic, bladder,
 CC prostate, endometrial, brain, kidney, or oesophagus, or a melanoma or
 CC sarcoma, premalignancy or carcinoma in-situ, preferably cervical
 CC dysplasia, cervical intraepithelial neoplasia, bronchial dysplasia,
 CC atypical hyperplasia of the breast, ductal carcinoma in-situ,
 CC colorectal adenoma, atypical endometrial hyperplasia, or Barrett's
 CC oesophagus, where the human is at risk for developing a malignancy or
 CC premalignancy or is known to have malignancy, premalignancy or
 CC carcinoma in situ. The method is also useful for treating a human with
 CC cancer for the telomerase-directed therapy, which comprises selecting the
 CC cancer for the therapy after detection of (I), for determining a
 CC need for diagnostic test in a human with malignancy or premalignancy
 CC and for monitoring a therapy administered to a human. (I) provides a
 CC marker which is utilised as a guide to whether adequate therapeutic
 CC effect has been achieved, or whether additional or more advanced therapy
 CC is required, and to assess prognosis in these patients. The method also
 CC allows identification or analysis, either quantitatively or
 CC qualitatively, of (I) in plasma or serum of humans during or following
 CC surgical procedures to remove premalignant or malignant lesions, and thus
 CC allow stratification of such patients as to their risk of residual
 CC cancer following surgery, and their need for further therapy or who has
 CC completed therapy as an early indicator or relapsed cancer, impending
 CC relapse, or treatment failure. The method allows the development and
 CC application of telomerase-specific therapy even when only premalignant
 CC tumours, early cancer, or occult cancer or metastasis such as following
 CC resection or in minimal residual disease are present. The present
 CC sequence represents a PCR primer for human telomerase-associated
 CC RNA template (hTR).
 XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 SQ

Query Match 100.0%; Score 15; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 15

AAD24246
ID AAD24246 standard; DNA; 26 BP.
XX
AC AAD24246;
XX
DT 07-MAR-2002 (first entry)
XX
DE Human telomerase (hTR) cDNA amplifying R3c downstream RT-PCR primer.
XX
KW Human; telomerase; TR; telomerase activity-related disease; therapy;
KW cancer; pregnancy; fertility; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
FN US6300110-B1.
XX
PD 09-OCT-2001.
XX
PF 23-DEC-1998; 98US-0220157.
XX
PR 09-SEP-1995; 95US-003492P.
PR 13-SEP-1996; 96US-0710249.
PR 05-JAN-1996; 96US-0583808.
XX
PA (GERO-) GERON CORP.
XX
PI Villeponteau B, Peng J, Andrews WH, Adams RR;
XX
DR WPI; 2002-033174/04.
XX
PT Peptide products of the human TPC2 and TPC3 gene are involved in
PT regulation of telomere length and activity are useful to diagnose and
PT treat telomere length and activity-related diseases -
XX
PS Example; Column 38; 60pp; English.
XX
CC The invention relates to methods and reagents for regulating telomere
CC length and for modulating telomerase activity in mammalian cells. The
CC invention also relates to purified, synthetic or recombinant peptides
CC such as TPC2 or TPC3 used for detecting regulators of telomere length
CC and telomerase activity in mammalian cells and for a variety of related
CC diagnostic and therapeutic purposes. The method is useful for screening,
CC diagnosing, monitoring and treating diseases and other conditions such as
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC The present sequence is a reverse transcription (RT) PCR primer
CC used for amplifying human telomerase (hTR) cDNA.
XX
SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

Search completed: June 23, 2003, 05:43:39
Job time : 100.989 secs

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OM nucleic - nucleic search, using sw model
Run on: June 23, 2003, 01:05:28 ; Search time 174.442 Seconds
(without alignments)
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- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	15	6	AR063834	AR063834 Sequence
2	15	100.0	19	6	AR063833	AR063833 Sequence
3	15	100.0	26	6	A94988	A94988 Sequence 2
4	15	100.0	26	6	AR016055	AR016055 Sequence
5	15	100.0	26	6	AR028786	AR028786 Sequence
6	15	100.0	26	6	AR059216	AR059216 Sequence
7	15	100.0	26	6	AR075527	AR075527 Sequence
8	15	100.0	26	6	AR161925	AR161925 Sequence
9	15	100.0	26	6	AX022187	AX022187 Sequence
10	15	100.0	26	6	AX033377	AX033377 Sequence
11	15	100.0	26	6	AX468455	AX468455 Sequence
12	15	100.0	26	6	BD011297	BD011297 Human tel
13	15	100.0	26	6	E36508	E36508 Method for
14	15	100.0	26	6	E37046	E37046 Human telom
15	15	100.0	26	6	I31770	I31770 Sequence 23
16	15	100.0	27	6	AR063850	AR063850 Sequence
17	15	100.0	27	6	AX317989	AX317989 Sequence
18	15	100.0	30	6	AR063832	AR063832 Sequence
19	15	100.0	30	6	AX465471	AX465471 Sequence
20	14	93.3	30	6	A84596	A84596 Sequence 6
21	14	93.3	30	6	AR079893	AR079893 Sequence
22	13	86.7	18	6	BD011244	BD011244 Human tel
23	13	86.7	18	6	E36993	E36993 Human telom
24	13	86.7	28	6	AX298137	AX298137 Sequence
25	12	80.0	17	6	AX099957	AX099957 Sequence
26	12	80.0	25	6	I04124	I04124 Sequence 8
27	12	80.0	26	6	AR000025	AR000025 Sequence
28	12	80.0	26	6	AR169136	AR169136 Sequence
29	12	80.0	26	6	AR202623	AR202623 Sequence
30	12	80.0	26	6	AX036237	AX036237 Sequence
31	12	80.0	30	6	I25474	I25474 Sequence 3
32	12	80.0	36	6	I04342	I04342 Sequence 6
33	12	80.0	39	6	E49124	E49124 Novel G pro
34	12	80.0	39	6	E50834	E50834 Novel G pro
35	11	73.3	11	6	AR063835	AR063835 Sequence
36	11	73.3	19	6	AX244257	AX244257 Sequence
37	11	73.3	21	6	AR193717	AR193717 Sequence
38	11	73.3	22	6	AR205029	AR205029 Sequence
39	11	73.3	22	6	AX082540	AX082540 Sequence
40	11	73.3	22	6	AX370655	AX370655 Sequence
41	11	73.3	23	6	AR112025	AR112025 Sequence
42	11	73.3	24	6	A91468	A91468 Sequence 10
43	11	73.3	24	6	AX085592	AX085592 Sequence
44	11	73.3	26	6	AR179447	AR179447 Sequence
45	11	73.3	27	6	AX175102	AX175102 Sequence

ALIGNMENTS

RESULT 1
AR063834
LOCUS AR063834 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5846723.
ACCESSION AR063834
VERSION AR063834.1 GI:5993142
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim N.Woo., Wu, F., Kealey J.T., Pruzan, R. and Weinrich, S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 10 08-DEC-1998;
FEATURES Location/Qualifiers

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source 1..15
BASE COUNT 5 a 3 c 4 g 3 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 1 GCTCTAGATGAACG 15

RESULT 2
LOCUS AR063833 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5846723.
ACCESSION AR063833
VERSION AR063833.1 GI:5993141
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 9 08-DEC-1998;
FEATURES Location/Qualifiers
source 1..19
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ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 1 GCTCTAGATGAACG 15

RESULT 3
LOCUS A94988 26 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 2 from Patent EP0926245.
ACCESSION A94988
VERSION A94988.1 GI:6779168
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Emrich,T.D.
TITLE Method for detection of carcinoma of the urinary bladder within a
JOURNAL urine sample
Patent: EP 0926245-A 2 30-JUN-1999;
ROCHE DIAGNOSTICS GMBH (DE)
FEATURES Location/Qualifiers
source 1..26
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/db_xref="taxon:32644"
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 4
LOCUS AR016055 26 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 23 from patent US 5776679.
ACCESSION AR016055
VERSION AR016055.1 GI:3972332
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 5
LOCUS AR028786 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5858777.
ACCESSION AR028786
VERSION AR028786.1 GI:5940759
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLE Methods and reagents for regulating telomere length and telomerase
JOURNAL activity
Patent: US 5858777-A 26 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 6
LOCUS AR059216 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5837857.
ACCESSION AR059216
VERSION AR059216.1 GI:5984793
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
```

TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 23 17-NOV-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 7
LOCUS AR075527 26 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5958680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Viliepointeau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 24 28-SEP-1999;
FEATURES Location/Qualifiers
source
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 8
LOCUS AR161925 26 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 23 from patent US 6258535.
ACCESSION AR161925
VERSION AR161925.1 GI:16228953
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Viliepointeau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 23 10-JUL-2001;
FEATURES Location/Qualifiers
source
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 9
LOCUS AX022187 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent EP0953042.
ACCESSION AX022187
VERSION AX022187.1 GI:10045855
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Andrews,W.H., Viliepointeau,B., Adams,R.R. and Feng,J.
TITLE Methods and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: EP 0953042-A 26 03-NOV-1999;
FEATURES Location/Qualifiers
source
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 10
LOCUS AX033377 26 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 9 from Patent WO0046601.
ACCESSION AX033377
VERSION AX033377.1 GI:10280151
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 9 10-AUG-2000;
FEATURES Location/Qualifiers
source
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 11
LOCUS AX468455 26 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 5 from Patent WO0218652.
ACCESSION AX468455
VERSION AX468455.1 GI:21901291
KEYWORDS

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Koprski, M.S. and Gocke, C.D.
 TITLE Method for detection of htr and htert telomerase-associated rna in
 JOURNAL plasma or serum
 Patent: WO 0218652-A 5 07-MAR-2002;
 Oncomedx, Inc. (US)
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 source Location/Qualifiers
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 /db_xref="taxon:9606" 7 t
 BASE COUNT 7 a 3 c 9 g
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 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db |||||
 RESULT 12
 BD011297
 LOCUS Human telomerase catalytic subunit. 26 bp DNA linear PAT 31-JAN-2002
 DEFINITION
 ACCESSION BD011297
 VERSION BD011297.1 GI:18639670
 KEYWORDS JP 2001081042-A/254.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE unclassified.
 AUTHORS Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,
 Harley, C.B. and Andrews, W.H.
 TITLE Human telomerase catalytic subunit
 JOURNAL Human telomerase catalytic subunit
 Patent: JP 2001081042-A 254 27-MAR-2001;
 GERON CORP, UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 2001081042-A/254
 PD 27-MAR-2001
 PF 27-JUL-2000 JP 2000227474
 PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR
 25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR
 09-MAY-1997 US 08/854050, 14-AUG-1997 US 08/911312 PR
 14-AUG-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI THOMAS
 R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
 MORIN,
 PI CALVIN B HARLEY, WILLIAM H ANDREWS
 PC A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,
 PC C07K5/10,
 PC C07K5/107, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12, PC
 C12N15/09,
 PC C12N1/02, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
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 CC Topology: Linear;
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 FT source 1. .26
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 /db_xref="taxon:32644" 7 t
 BASE COUNT 7 a 3 c 9 g
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 QY 1 GCTCTAGATGAACG 15
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 RESULT 13
 BD011297
 LOCUS Human telomerase catalytic subunit. 26 bp DNA linear PAT 18-JUN-2001
 DEFINITION
 ACCESSION BD011297
 VERSION BD011297.1 GI:13022705
 KEYWORDS JP 1999243995-A/2.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE artificial sequences.
 AUTHORS Thomas, E.
 TITLE Method for detecting bladder cancer in urine samples
 JOURNAL Patent: JP 1999243995-A 2 14-SEP-1999;
 ROCHE DIAGNOSTICS GMBH
 COMMENT OS Artificial Sequence
 PN JP 1999243995-A/2
 PD 14-SEP-1999
 PF 22-DEC-1998 JP 1998365689
 PR 22-DEC-1997 DE 19757300.2
 PI THOMAS ENRIHI
 PC C12Q1/68//C12N1/00
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 /db_xref="taxon:32630" 7 t
 BASE COUNT 7 a 3 c 9 g
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 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACG 15
 Db |||||
 RESULT 14
 BD011297
 LOCUS Human telomerase catalytic subunit promoter. 26 bp DNA linear PAT 18-JUN-2001
 DEFINITION
 ACCESSION BD011297
 VERSION BD011297.1 GI:13023009
 KEYWORDS JP 1999253177-A/254.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE unclassified.
 AUTHORS Thomas, R.S., Jochim, R., Toru, N., Karen, B.C., Greg, B.M.,
 Calvin, B.H. and William, H.A.
 TITLE Human telomerase catalytic subunit promoter
 JOURNAL Patent: JP 1999253177-A 254 21-SEP-1999;
 JERON CORP, UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 1999253177-A/254
 PD 21-SEP-1999
 PF 15-OCT-1998 JP 1998320169
 PR 01-OCT-1996 US 08/724.643, 18-APR-1997 US 08/844.419, PR
 25-APR-1997 US 08/846.017, 06-MAY-1997 US 08/851.843, PR
 09-MAY-1997 US 08/854.050, 14-AUG-1997 US 08/911.312, PR

Search completed: June 23, 2003, 06:34:21
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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292.710 Million cell updates/sec

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Perfect score: 11
Sequence: 1 GCTCTAGATG 11

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Gapop 10.0, Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	11	100.0	18	9	US-10-325-810-543
3	11	100.0	21	1	PCT-US03-05708-27
4	11	100.0	21	1	PCT-US03-05708-202
5	11	100.0	21	1	PCT-US03-04088-539
6	11	100.0	21	1	PCT-US03-04088-543
7	11	100.0	21	1	PCT-US03-04088-547
8	11	100.0	21	1	PCT-US03-04088-551
9	11	100.0	21	1	PCT-US03-04088-555
10	11	100.0	21	1	PCT-US03-04088-559
11	11	100.0	21	10	US-10-374-366-27
12	11	100.0	21	10	US-10-374-366-202
13	11	100.0	22	9	US-10-188-523B-5
14	11	100.0	22	9	US-10-188-523C-5
15	11	100.0	23	1	PCT-US03-04088-520
16	11	100.0	23	1	PCT-US03-04088-521
17	11	100.0	23	9	US-10-310-188-36216
18	11	100.0	24	5	US-09-807-809A-5
19	11	100.0	25	7	US-09-954-445A-66031
20	11	100.0	25	9	US-10-355-577-393144

21	11	100.0	25	9	US-10-355-577-396066
22	11	100.0	25	9	US-10-355-577-924166
23	11	100.0	25	12	US-60-427-808-6866
24	11	100.0	25	12	US-60-427-808-62369
25	11	100.0	25	12	US-60-427-808-104137
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28	11	100.0	25	12	US-60-427-808-301228
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35	11	100.0	25	12	US-60-427-808-681848
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38	11	100.0	25	12	US-60-427-836-248462
39	11	100.0	25	12	US-60-427-836-248463
40	11	100.0	25	12	US-60-427-836-280388
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44	11	100.0	26	1	PCT-US02-11134-11
45	11	100.0	26	1	PCT-US02-11134-13

ALIGNMENTS

RESULT 1

US-09-721-456-543

; Sequence 543, Application US/09721456

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/721,456

; FILING DATE: 22-Nov-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 35,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 543:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "antisense hTERT molecule"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-456-543

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Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 2
US-10-325-810-543
; Sequence 543, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ausenhuis, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-002620US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 543:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "antisense hTERT molecule"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-10-325-810-543

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCTCTAGATG 11

RESULT 3
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; Sequence 27, Application PC/TUS0305708
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Company, Inc.
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/05708
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer 18-5'
PCT-US03-05708-27

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Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

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RESULT 4
PCT-US03-05708-202
; Sequence 202, Application PC/TUS0305708
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Company, Inc.
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/05708
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 202
; TYPE: DNA
; ORGANISM: Rhodospiridium glutinis
PCT-US03-05708-202

Query Match          100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1  GCTCTAGAATG 11
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Db          3  GCTCTAGAATG 13

RESULT 5
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region

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Db          3  GCTCTAGAATG 13

RESULT 6
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

QY          1  GCTCTAGAATG 11
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Db          19 GCTCTAGAATG 9

Query Match          100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1  GCTCTAGAATG 11
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Db          19 GCTCTAGAATG 9

RESULT 7
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
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; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 547
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: Description of Artificial Sequence: 5' sense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety
; PCT-US03-04088-547

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
Db 19 GCTCTAGATG 9

RESULT 8
PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

```

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; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; PCT-US03-04088-551

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
Db 1 GCUCUAGAAUG 11

RESULT 9
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

```

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; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine

```

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-555
Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
Db 19 GCTCTAGATG 9
RESULT 10
PCT-US03-04088-559
; Sequence 559, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)..(9)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559

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Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTAGAATG 11
||:|||||
Db 1 GCUCUAGAUG 11

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RESULT 11
US-10-374-366-27
; Sequence 27, Application US/10374366
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 US NA
; CURRENT APPLICATION NUMBER: US/10/374,366
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer 18-5'
US-10-374-366-27

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Query Match 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTAGAATG 11
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Db 3 GCTCTAGAATG 13

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RESULT 12
US-10-374-366-202
; Sequence 202, Application US/10374366
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 US NA

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; CURRENT APPLICATION NUMBER: US/10/374,366
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 202
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Rhodospiridium glutinis
US-10-374-366-202

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Query Match 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTAGAATG 11
||:|||||
Db 3 GCTCTAGAATG 13

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RESULT 13
US-10-188-523B-5
; Sequence 5, Application US/10188523B
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US DIVCIP
; CURRENT APPLICATION NUMBER: US/10/188,523B
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-188-523B-5

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Query Match 100.0%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTAGAATG 11
||:|||||
Db 3 GCTCTAGAATG 13

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RESULT 14
US-10-188-523C-5
; Sequence 5, Application US/10188523C
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009-CIP
; CURRENT APPLICATION NUMBER: US/10/188,523C
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: MICROSOFT OFFICE 97
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: primer
US-10-188-523C-5

Query Match 100.0%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATG 11
|||
Db 3 GCTCTAGAAATG 13

RESULT 15
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 100.0%; Score 11; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATG 11
|||
Db 23 GCTCTAGAAATG 13

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Job time : 264.081 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 453.88 Seconds
 (without alignments)
 292.710 Million cell updates/sec

Title: US-08-770-564A-9
 Perfect score: 19
 Sequence: 1 GCTCTAGATGACCGTGG 19

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 7850393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
 Maximum DB seq length: 50

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	100.0	21	1	PCT-US03-04088-539
C 2	19	100.0	21	1	PCT-US03-04088-539
C 3	19	100.0	21	1	PCT-US03-04088-547
C 4	19	100.0	21	1	PCT-US03-04088-551
C 5	19	100.0	21	1	PCT-US03-04088-555
C 6	19	100.0	21	1	PCT-US03-04088-559
C 7	19	100.0	23	1	PCT-US03-04088-520
C 8	19	100.0	23	1	PCT-US03-04088-521
9	19	100.0	26	9	US-09-721-456-598
10	19	100.0	26	9	US-10-325-810-598
11	19	100.0	26	9	US-10-359-935-23
12	19	100.0	30	10	US-10-330-872-5
13	19	100.0	30	10	US-10-330-872A-5
C 14	17	89.5	21	1	PCT-US03-04088-538
C 15	17	89.5	21	1	PCT-US03-04088-542
C 16	17	89.5	21	1	PCT-US03-04088-546
C 17	17	89.5	21	1	PCT-US03-04088-550
C 18	17	89.5	21	1	PCT-US03-04088-554
C 19	17	89.5	21	1	PCT-US03-04088-558
20	16.4	86.3	18	6	US-09-721-456-543

21	16.4	86.3	18	9	US-10-325-810-543	Sequence 543, App
22	14.8	77.9	25	9	US-10-355-577-751232	Sequence 751232, A
C 23	14.4	75.8	25	9	US-10-355-577-70333	Sequence 70333, A
24	14.2	74.7	25	7	US-09-954-445A-54976	Sequence 54976, A
C 25	14	73.7	23	9	US-10-310-188-36216	Sequence 36216, A
26	14	73.7	24	8	US-10-442-506-39	Sequence 39, Appl
27	14	73.7	25	12	US-60-427-808-952738	Sequence 952738, A
28	14	73.7	25	13	US-60-469-545-13722	Sequence 13722, A
C 29	14	73.7	25	13	US-60-469-545-222991	Sequence 222991, A
C 30	13.8	72.6	25	9	US-10-098-263B-64498	Sequence 64498, A
31	13.8	72.6	25	9	US-10-355-577-44115	Sequence 44115, A
C 32	13.8	72.6	25	9	US-10-355-577-45101	Sequence 45101, A
C 33	13.8	72.6	25	9	US-10-355-577-134105	Sequence 134105, A
C 34	13.8	72.6	25	12	US-60-427-808-304013	Sequence 304013, A
C 35	13.8	72.6	25	12	US-60-427-808-666732	Sequence 666732, A
C 36	13.8	72.6	25	12	US-60-427-808-738286	Sequence 738286, A
37	13.8	72.6	25	12	US-60-427-836-279457	Sequence 279457, A
C 38	13.4	70.5	25	9	US-10-355-577-173196	Sequence 173196, A
C 39	13.4	70.5	25	9	US-10-355-577-544182	Sequence 544182, A
C 40	13.4	70.5	25	9	US-10-355-577-981444	Sequence 981444, A
41	13.4	70.5	25	12	US-60-417-190-74827	Sequence 74827, A
42	13.4	70.5	25	12	US-60-417-190-74828	Sequence 74828, A
43	13.4	70.5	25	12	US-60-417-190-74829	Sequence 74829, A
44	13.4	70.5	25	12	US-60-417-190-74830	Sequence 74830, A
45	13.4	70.5	25	12	US-60-417-190-74831	Sequence 74831, A

ALIGNMENTS

RESULT 1
 PCT-US03-04088-539/c
 ; Sequence 539, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04089
 ; PRIOR FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626.
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 539
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
 ; NAME/KEY: misc feature
 ; LOCATION: (20)..(21)
 ; OTHER INFORMATION: n stands for thymidine
 PCT-US03-04088-539

Query Match 100.0%; Score 19; DB 1; Length 21;

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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
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Db 19 GCTCTAGATGAACGGTGG 1

RESULT 2
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety
PCT-US03-04088-547

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
    |||:|||||:|||||:|||||
Db 19 GCTCTAGATGAACGGTGG 1

RESULT 4
PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-543

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.2;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
    |||:|||||:|||||:|||||
Db 1 GCUCUAGAUGAAGCGUGG 19

RESULT 3
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17

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;; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 551
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
;; OTHER INFORMATION: antisense region
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2)..(5)
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (10)..(10)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (14)..(14)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (17)..(17)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (20)..(21)
;; OTHER INFORMATION: n stands for thymidine
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (20)..(20)
;; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-551
Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 2.2;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTTAGAATGACCGTGG 19
Db 1 GCUCUAGAAUGAACGGG 19
RESULT 5
PCT-US03-04088-555/c
;; Sequence 555, Application PC/TUS0304088
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
;; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

;; FILE REFERENCE: 02-708-A (400/080)
;; CURRENT APPLICATION NUMBER: PCT/US03/04088
;; CURRENT FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/396,600
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 60/386,782
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/406,784
;; PRIOR FILING DATE: 2002-08-29
;; PRIOR APPLICATION NUMBER: US 60/408,378
;; PRIOR FILING DATE: 2002-09-05
;; PRIOR APPLICATION NUMBER: US 60/409,293
;; PRIOR FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: US 60/440,129
;; PRIOR FILING DATE: 2003-01-15
;; NUMBER OF SEQ ID NOS: 626
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 555
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
;; OTHER INFORMATION: region
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(2)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (3)..(3)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (4)..(5)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (6)..(6)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (7)..(9)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (10)..(10)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (11)..(14)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (15)..(18)
;; OTHER INFORMATION: 2'-deoxy
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (19)..(19)
;; OTHER INFORMATION: 2'-deoxy-2'-fluoro
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (20)..(21)
;; OTHER INFORMATION: n stands for thymidine
;; FEATURE:


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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
Db 23 GCTCTAGAAATGAACGGTGG 5

RESULT 8
PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 521
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 100.0%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
Db 21 GCTCTAGAAATGAACGGTGG 3

RESULT 9
US-09-721-456-598
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

```

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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-09-721-456-598
SEQUENCE DESCRIPTION: SEQ ID NO: 598:

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 10
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

```

/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 23-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ausenhus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 598:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..26
/ OTHER INFORMATION: /note="R3c primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGAATGACGGTGG 19
Db 5 GCTCTAGAATGACGGTGG 23
RESULT 11

US-10-359-935-23
/ Sequence 23, Application US/10359935
/ GENERAL INFORMATION:
/ APPLICANT: Villeponteau, Bryant
/ Feng, Junli
/ Funk, Walter
/ Andrews, William H.
/ TITLE OF INVENTION: Mammalian Telomerase
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/359,935
/ FILING DATE: 07-Feb-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/057,351
/ FILING DATE: 08-APR-1994
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 07-JUL-1994
/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ APPLICATION NUMBER: US 08/472,802
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 015389-000821US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23
Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGAATGACGGTGG 19
Db 5 GCTCTAGAATGACGGTGG 23
RESULT 12
US-10-330-872-5
/ Sequence 5, Application US/10330872
/ GENERAL INFORMATION:
/ APPLICANT: Geron Corporation
/ APPLICANT: Weinrich, Scott
/ APPLICANT: Atkinson III, Edward
/ APPLICANT: Lichtsteiner, Serge
/ APPLICANT: Vasserot, Alain
/ APPLICANT: Pruzan, Ronald
/ TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
/ TITLE OF INVENTION: Inhibitors
/ FILE REFERENCE: 011/006C


```

; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAAATGAACGGTGG 19
      |||||
Db      1 GCTCTAGAAATGAACGGTGG 19

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGAAATGAACGGTGG 19
      |||||
Db      1 GCTCTAGAAATGAACGGTGG 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James

```

```

; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-538

Query Match      89.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TCTAGAAATGAACGGTGG 19
      |||||
Db      19 TCTAGAAATGAACGGTGG 3

RESULT 15
PCT-US03-04088-542
; Sequence 542, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: Expression Using Short Interfering RNA (siRNA)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15

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; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 542
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-542

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Query Match      89.5%; Score 17; DB 1; Length 21;
Best Local Similarity 76.5%; Pred. No. 28;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 TCTAGATGAACGGTGG 19
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Db      1 UCUAGAAUGAACGGUGG 17

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Search completed: June 26, 2003, 04:15:18
Job time : 454.188 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1612.2 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGATGACCGTGG 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	100.0	19	11	US-08-770-564A-9
3	19	100.0	25	16	US-09-250-336A-4
4	19	100.0	25	25	US-09-642-177-4
5	19	100.0	26	1	PCT-US96-14679-27
6	19	100.0	26	1	PCT-US96-14679A-27
7	19	100.0	26	1	PCT-US99-03302-4
8	19	100.0	26	1	PCT-US99-07533-4
9	19	100.0	26	1	PCT-US99-07533-4
10	19	100.0	26	6	US-08-272-102-23
11	19	100.0	26	7	US-08-387-524-19
12	19	100.0	26	8	US-08-472-802A-24
13	19	100.0	26	8	US-08-472-802B-24
14	19	100.0	26	8	US-08-482-115A-23
15	19	100.0	26	9	US-08-520-550-19
16	19	100.0	26	9	US-08-521-634-41
17	19	100.0	26	10	US-08-660-678-23
18	19	100.0	26	13	US-08-911-312-23
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20	19	100.0	26	13	US-08-912-951-312
21	19	100.0	26	13	US-08-973-589-17

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 23 19 100.0 26 14 US-09-057-351-23
 24 19 100.0 26 16 US-09-216-847-2
 25 19 100.0 26 16 US-09-250-336-4
 26 19 100.0 26 16 US-09-259-943-45
 27 19 100.0 26 18 US-09-402-181A-598
 28 19 100.0 26 18 US-09-402-181B-598
 29 19 100.0 26 18 US-09-432-503-598
 30 19 100.0 26 25 US-09-653-573-5
 31 19 100.0 26 29 US-09-721-477-598
 32 19 100.0 26 29 US-09-721-506-598
 33 19 100.0 26 33 US-09-890-567-9
 34 19 100.0 26 33 US-09-895-606-26
 35 19 100.0 26 38 US-10-044-539-312
 36 19 100.0 26 38 US-10-044-692-312
 37 19 100.0 27 1 PCT-US97-23619-26
 38 19 100.0 30 1 PCT-US97-23619-8
 39 19 100.0 30 9 US-08-510-736-5
 40 19 100.0 30 11 US-08-770-564A-8
 41 19 100.0 30 21 US-09-540-119B-10
 42 19 100.0 30 28 US-09-717-828A-5
 43 19 100.0 30 28 US-09-717-828B-5
 44 19 100.0 30 28 US-09-717-829A-5
 45 19 100.0 30 34 US-09-903-461-2

ALIGNMENTS

RESULT 1
 PCT-US97-23619-9
 ; Sequence 9, Application PC/TUS9723619
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/23619
 ; FILING DATE: Not yet assigned
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,564
 ; FILING DATE: 20-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,565
 ; FILING DATE: 20-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 15389-27PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:

Sequence 598, App
 Sequence 23, Appl
 Sequence 2, Appl
 Sequence 4, Appl
 Sequence 45, Appl
 Sequence 598, App
 Sequence 598, App
 Sequence 5, Appl
 Sequence 598, App
 Sequence 26, Appl
 Sequence 312, App
 Sequence 26, Appl
 Sequence 8, Appl
 Sequence 5, Appl
 Sequence 5, Appl
 Sequence 5, Appl
 Sequence 2, Appl

LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..19
 OTHER INFORMATION: /note= "oligo 2lab"
 PCT-US97-23619-9
 Query Match 100.0%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred.No. 7.2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
 Db 1 GCTCTAGATGACGGTGG 19
 RESULT 2
 US-08-770-564A-9
 ; Sequence 9, Application US/08770564A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ron
 ; APPLICANT: Weinrich, Scott L.
 ; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,564A
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-770-564A-9

Query Match 100.0%; Score 19; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred.No. 7.2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGACGGTGG 19
 Db 1 GCTCTAGATGACGGTGG 19
 RESULT 3
 US-09-250-336A-4

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; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT APPLICATION NUMBER: US/09/250,336A
; CURRENT FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

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Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 4 GCTCTAGAATGAACGGTGG 22

RESULT 4
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 09/250,336
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match      100.0%; Score 19; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 4 GCTCTAGAATGAACGGTGG 22

RESULT 5
PCT-US96-14679-27
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; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match      100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATGAACGGTGG 19
Db 5 GCTCTAGAATGAACGGTGG 23

RESULT 6
PCT-US96-14679A-27
; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERASE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       5  GCTCTAGATGAACGGTGG 23

RESULT 9
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match      100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCTAGATGAACGGTGG 19
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Db       5  GCTCTAGATGAACGGTGG 23

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US-08-272-102-23
; Sequence 23, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1 0 Version #1 25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-08-387-524-19
; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-387-524-19

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; APPLICANT: Mammalian Telomerase
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23
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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-524-19

Query Match 100.0%; Score 19; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; APPLICANT: Mammalian Telomerase
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 5 GCTCTAGATGAACGGTGG 23
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RESULT 13
US-08-472-802B-24
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-24

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 14
US-08-482-115A-23
; Sequence 23, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115A-23

Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 15
US-08-520-550-19
; Sequence 19, Application US/08520550
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-520-550-19

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Query Match      100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGAAATGAACGGTGG 19
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Db      5 GCTCTAGAAATGAACGGTGG 23

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Search completed: June 25, 2003, 06:20:26
Job time : 1612.81 secs

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		Match	Length				
1	19	100.0	26	9	US-10-044-532-312	Sequence 312, App	
2	19	100.0	26	9	US-10-044-539-312	Sequence 312, App	
3	19	100.0	26	10	US-09-057-351-23	Sequence 23, App	
C	13.8	72.6	25	9	US-10-098-253B-6498	Sequence 6498, A	
5	13.8	72.6	31	9	US-10-139-483-3	Sequence 3, Appl	
6	13.2	69.5	25	9	US-10-098-263B-51583	Sequence 51583, A	
7	13.2	69.5	26	9	US-09-952-522B-19	Sequence 19, Appl	
8	13.2	69.5	40	9	US-10-090-182A-255	Sequence 255, App	
9	13.2	69.5	41	9	US-10-090-182A-234	Sequence 234, App	
C	13.2	69.5	45	9	US-10-090-182A-235	Sequence 235, App	
10	13.2	69.5	45	9	US-10-090-182A-409	Sequence 409, App	
11	13.2	69.5	45	9	US-10-090-182A-118949	Sequence 118949, A	
C	13	68.4	28	10	US-09-844-006A-3	Sequence 3, Appl	
14	12.8	67.4	25	9	US-10-215-112-12114	Sequence 12114, A	
15	12.8	67.4	25	9	US-10-215-112-12846	Sequence 12846, A	
16	12.8	67.4	25	9	US-10-098-263B-20598	Sequence 20598, A	
C	12.8	67.4	25	9	US-10-098-263B-53938	Sequence 53938, A	
17	12.8	67.4	25	9	US-10-098-263B-69798	Sequence 69798, A	
18	12.8	67.4	31	9	US-09-848-754A-7103	Sequence 7103, App	
19	12.8	67.4	31	9	US-09-848-754A-7103	Sequence 7103, App	

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
Db 5 GCTCTAGATGACGGTGG 23

RESULT 2

US-10-044-539-312

Sequence 312, Application US/10044539

Publication No. US20030100093A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
Db 5 GCTCTAGATGACGGTGG 23

RESULT 3

US-09-057-351-23

Sequence 23, Application US/09057351

Patent No. US20010034439A1

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,351

FILING DATE: 08-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 19; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.72; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 4
US-10-098-263B-64498/c
; Sequence 64498, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64498
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64498

Query Match 72.6%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCTAGATGAACGGTGG 19
Db 23 TCTAGATGAACGTAG 7

RESULT 5
US-10-139-483-3
; Sequence 3, Application US/10139483
; Publication No. US200305266A1
; GENERAL INFORMATION:
; APPLICANT: Beeley, Nigel R
; APPLICANT: Behan, Dominic P
; APPLICANT: Chalmers, Derek T
; APPLICANT: Menzaghi, Frederique
; APPLICANT: Strah-Pleyvet, Sonja
; TITLE OF INVENTION: Small Molecule Modulators Of G Protein-Coupled Receptor
; TITLE OF INVENTION: Six
; FILE REFERENCE: AREN0058
; CURRENT APPLICATION NUMBER: US/10/139,483
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/513,838
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/364,425
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-139-483-3

Query Match 72.6%; Score 13.8; DB 9; Length 31;
Best Local Similarity 88.2%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTCTAGATGAACGGTG 18
Db 4 CTCTAGATGACGGGTG 20

RESULT 6
US-10-098-263B-51583
; Sequence 51583, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-51583

Query Match 69.5%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTCTAGATGAACGGTGG 19
Db 7 CTCTAGATCAACGGTGG 24

RESULT 7
US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Lull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer
US-09-952-522B-19

Query Match 69.5%; Score 13.2; DB 9; Length 26;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTG 18
Db 7 GCTCTAGATGAACGGTG 24

Db 1 GCTCTAGATGAAGACTG 18

RESULT 8

US-10-090-182A-255
; Sequence 255, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mairé H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kuman
Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
Corporate Patent Dept. Mail Zone 04E
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,182A
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/764,114
FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993

APPLICATION NUMBER: 08/411,795
FILING DATE: 04-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C2713/12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257

TELEFAX: (736)737-6257
INFORMATION FOR SEQ ID NO: 255:

SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
SEQUENCE DESCRIPTION: SEQ ID NO: 255:

US-10-090-182A-255
Query Match 69.5%; Score 13.2; DB 9; Length 40;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAAGACTG 18

Db 12 GCTCTATATGATCGATG 29

RESULT 9

US-10-090-182A-234
; Sequence 234, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mairé H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kuman
Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
Corporate Patent Dept. Mail Zone 04E
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,182A
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/764,114
FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993

APPLICATION NUMBER: 08/411,795
FILING DATE: 04-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C2713/12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257

TELEFAX: (736)737-6257
INFORMATION FOR SEQ ID NO: 234:

SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
SEQUENCE DESCRIPTION: SEQ ID NO: 234:

US-10-090-182A-234
Query Match 69.5%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAAGACTG 18

Db 12 GCTCTATATGATCGATG 29

RESULT 10

US-10-090-182A-235/c
; Sequence 235, Application US/10090182A
; Publication No. US20030103936A1
; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mair H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Oline, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides

NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
Corporate Patent Dept. Mail Zone 04E
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,182A
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/764,114
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/411,795
FILING DATE: 04-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C2713/12
TELEPHONE: (636)737-6257
TELEFAX: (736)737-6257
INFORMATION FOR SEQ ID NO: 235:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
SEQUENCE DESCRIPTION: SEQ ID NO: 235:

US-10-090-182A-235
Query Match 69.5%; Score 13.2; DB 9; Length 45;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTG 18
|||||
Db 38 GCTCTATAATGATCGATG 21

RESULT 11
US-10-090-182A-409/c
; Sequence 409, Application US/10090182A

Publication No. US20030103936A1
; GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mair H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Oline, Peter O.
; Paik, Kuman
; Thomas, John W.

TITLE OF INVENTION: Methods of Ex-vivo Expansion of
; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple
; Mutation Polypeptides

NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
Corporate Patent Dept. Mail Zone 04E
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,182A
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/764,114
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/411,795
FILING DATE: 04-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C2713/12
TELEPHONE: (636)737-6257
TELEFAX: (736)737-6257
INFORMATION FOR SEQ ID NO: 409:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
SEQUENCE DESCRIPTION: SEQ ID NO: 409:

US-10-090-182A-409
Query Match 69.5%; Score 13.2; DB 9; Length 45;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTG 18
|||||
Db 38 GCTCTATAATGATCGATG 21

RESULT 12
US-10-090-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

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; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-098-263B-118949

Query Match      68.4%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAACG 15
Db 20 TCTAGATGAACG 8

RESULT 13
US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match      68.4%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAAG 13
Db 1 GCTCTAGATGAAG 13

RESULT 14
US-10-215-112-12114/c
; Sequence 12114, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12114
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12114

Query Match      67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGG 16
Db 21 GCTCTAGATGAACGG 6

RESULT 15
US-10-215-112-12846
; Sequence 12846, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12846

Query Match      67.4%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTAGATGAACGGTGG 19
Db 5 CTCGATGAACGGTGG 20

Search completed: June 25, 2003, 22:25:07
Job time : 58.757 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 28.8406 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-9
Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	2	US-08-770-565-9
2	19	100.0	26	1	US-08-330-123A-23
3	19	100.0	26	1	US-08-482-115B-23
4	19	100.0	26	2	US-08-660-678A-23
5	19	100.0	26	2	US-08-710-249-26
6	19	100.0	26	2	US-08-485-778-19
7	19	100.0	26	2	US-08-472-802C-24
8	19	100.0	26	3	US-08-520-550A-19
9	19	100.0	26	3	US-08-998-443-23
10	19	100.0	26	4	US-08-974-549A-598
11	19	100.0	26	4	US-09-060-523-23
12	19	100.0	26	4	US-09-220-157A-26
13	19	100.0	26	4	US-09-286-959B-4
14	19	100.0	26	4	US-09-580-517-23
15	19	100.0	27	2	US-08-770-565-26
16	19	100.0	30	2	US-08-770-565-8
17	18	94.7	30	2	US-08-833-377-6
18	16.4	86.3	18	4	US-08-974-549A-543
19	15.8	83.2	27	3	US-08-630-172-24
20	15.8	83.2	27	4	US-09-375-419-24
21	15.4	81.1	42	1	US-08-439-813-2
22	15.4	81.1	42	5	PCT-US96-05291A-2
23	15	78.9	15	2	US-08-770-565-10
24	13.8	72.6	31	4	US-09-513-838-3
25	13.2	69.5	40	1	US-08-411-795B-255
26	13.2	69.5	40	1	US-08-469-319A-255
27	13.2	69.5	40	4	US-08-764-114-255

28 13.2 69.5 40 4 US-08-469-419-255 Sequence 255, App
29 13.2 69.5 41 1 US-08-411-795B-234 Sequence 234, App
30 13.2 69.5 41 1 US-08-469-319A-234 Sequence 234, App
31 13.2 69.5 41 4 US-08-764-114-234 Sequence 234, App
32 13.2 69.5 41 4 US-08-469-419-234 Sequence 234, App
33 13.2 69.5 45 1 US-08-411-795B-235 Sequence 235, App
34 13.2 69.5 45 1 US-08-411-795B-409 Sequence 409, App
35 13.2 69.5 45 1 US-08-469-319A-235 Sequence 235, App
36 13.2 69.5 45 1 US-08-469-319A-409 Sequence 409, App
37 13.2 69.5 45 4 US-08-764-114-235 Sequence 235, App
38 13.2 69.5 45 4 US-08-764-114-409 Sequence 409, App
39 13.2 69.5 45 4 US-08-469-419-235 Sequence 235, App
40 13.2 69.5 45 4 US-08-469-419-409 Sequence 409, App
41 12.8 67.4 48 2 US-09-273-839A-3 Sequence 9, Appli
42 12.4 65.3 23 4 US-08-813-940-12 Sequence 12, Appli
43 12.4 65.3 25 2 US-08-480-604A-16 Sequence 16, Appli
44 12.4 65.3 26 1 US-08-480-604A-16 Sequence 16, Appli
45 12.4 65.3 26 2 US-08-405-496A-16 Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19

```
Db      1 GCTCTAGAAATGAACGGTGG 19
|||||
RESULT 2
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match      100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACGGTGG 19
|||||
Db      5 GCTCTAGAAATGAACGGTGG 23
|||||

RESULT 4
US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 5

US-08-710-249-26
Sequence 26, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-710-249-26
Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 6

US-08-485-778-19
Sequence 19, Application US/08485778
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel Athena
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 7

US-08-472-802C-24
 ; Sequence 24, Application US/08472802C
 ; Patent No. 5958680
 ; GENERAL INFORMATION:
 ; APPLICANT: Villeponteau, Bryant
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Mammalian Telomerase
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,802C
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/330,123
 ; FILING DATE: 27-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15389-000820
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-472-802C-24

Query Match 100.0%; Score 19; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 8

US-08-520-550A-19
 ; Sequence 19, Application US/08520550A
 ; Patent No. 6013468
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrews, William H.
 ; APPLICANT: Avilion, Ariel A.
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Greider, Carol

; APPLICANT: Marhuenda, Maria A. B.
 ; APPLICANT: Villeponteau, Bryant
 ; TITLE OF INVENTION: RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/520,550A
 ; FILING DATE: 29-AUG-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/387,524
 ; FILING DATE: 13-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/330,123
 ; FILING DATE: 27-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-520-550A-19

Query Match 100.0%; Score 19; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 9

US-08-998-443-23
 ; Sequence 23, Application US/08998443
 ; Patent No. 6054575
 ; GENERAL INFORMATION:
 ; APPLICANT: Villeponteau, Bryant
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Mammalian Telomerase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-998-443-23

Query Match 100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 10
US-08-974-549A-598
; Sequence 598, Application US/08/74549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
;
US-08-974-549A-598

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-09-060-523-23
; Sequence 23, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
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/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/060,523
/ FILING DATE: 14-APR-1998
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/660,678
/ FILING DATE: 05-JUN-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 07-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 015389-00081305
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
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/ US-09-060-523-23
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/ Query Match 100.0%; Score 19; DB 4; Length 26;
/ Best Local Similarity 100.0%; Pred. No. 0.14;
/ Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ QY 1 GCTCTAGATGAACGGTGG 19
/ Db 5 GCTCTAGATGAACGGTGG 23
/
/ RESULT 12
/ US-09-230-157A-26
/ Sequence 26, Application US/09220157A
/ Patent No. 6300110
/ GENERAL INFORMATION:
/ APPLICANT: Villeponteau, Bryant
/ APPLICANT: Feng, Junli
/ APPLICANT: Andrews, William H.
/ APPLICANT: Adams, Robert R.
/ TITLE OF INVENTION: Methods and Reagents for Regulating
/ NUMBER OF INVENTION: Telomere Length and Telomerase Activity
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/220,157A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US/08/710,249
/ FILING DATE: 13-SEP-1996
/ APPLICATION NUMBER: US 08/583,808
/ FILING DATE: 05-JAN-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/003,492
/ FILING DATE: 08-SEP-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 015389-00122005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
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/ US-09-220-157A-26
/
/ Query Match 100.0%; Score 19; DB 4; Length 26;
/ Best Local Similarity 100.0%; Pred. No. 0.14;
/ Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 GCTCTAGATGAACGGTGG 19
/ Db 5 GCTCTAGATGAACGGTGG 23
/
/ RESULT 13
/ US-09-286-959B-4
/ Sequence 4, Application US/09286959B
/ Patent No. 6300131
/ GENERAL INFORMATION:
/ APPLICANT: Johns Hopkins University
/ APPLICANT: Greider, Carol W.
/ APPLICANT: Le, Siyuan
/ TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
/ FILE REFERENCE: 07265/157001
/ CURRENT APPLICATION NUMBER: US/09/286,959B
/ CURRENT FILING DATE: 1999-04-06
/ PRIOR APPLICATION NUMBER: 60/080,783
/ PRIOR FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 26
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
/
/ US-09-286-959B-4
/
/ Query Match 100.0%; Score 19; DB 4; Length 26;
/ Best Local Similarity 100.0%; Pred. No. 0.14;
/ Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 GCTCTAGATGAACGGTGG 19
/ Db 5 GCTCTAGATGAACGGTGG 23
/
/ RESULT 14
/ US-09-580-517-23
/ Sequence 23, Application US/09580517
/ Patent No. 6320039
/ GENERAL INFORMATION:
/ APPLICANT: VILLEPONTEAU, Bryant
/ FUNK, Junli
/ FUNK, Walter
```

ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 15
US-08-770-565-26
Sequence 26, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-26

Query Match 100.0%; Score 19; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

Search completed: June 25, 2003, 00:24:39
Job time : 28.8406 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 979.598 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

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Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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3: em_estin:*
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8: em_htc:*
9: gb_est1:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	10	52.6	29	17	TA264G10Q
5	10	52.6	34	10	AV964763
6	10	52.6	46	9	AA681423

7	10	52.6	49	17	BH791685
8	9	47.4	22	9	AU259636
9	9	47.4	24	17	AZ662500
10	9	47.4	25	9	AI763346
11	9	47.4	27	9	AU254302
12	9	47.4	27	17	BH812447
13	9	47.4	27	17	BH849811
14	9	47.4	27	17	TA349802P
15	9	47.4	30	9	AU257604
16	9	47.4	31	9	AI032592
17	9	47.4	31	17	TA106A06P
18	9	47.4	34	12	BG339578
19	9	47.4	34	12	BG340055
20	9	47.4	34	17	TA182F12P
21	9	47.4	36	12	BE797241
22	9	47.4	36	17	AZ812974
23	9	47.4	38	17	AZ786040
24	9	47.4	40	12	BG563012
25	9	47.4	41	9	AU258962
26	9	47.4	41	17	AZ775318
27	9	47.4	41	17	BH863752
28	9	47.4	41	17	BH863753
29	9	47.4	41	17	BH864990
30	9	47.4	42	12	BF732142
31	9	47.4	42	12	BG613445
32	9	47.4	42	14	CO1062
33	9	47.4	43	9	AA445326
34	9	47.4	43	17	AZ456311
35	9	47.4	44	17	AZ435397
36	9	47.4	44	17	BH624958
37	9	47.4	44	17	AL757115
38	9	47.4	45	17	AQ026252
39	9	47.4	46	17	AZ812338
40	9	47.4	46	17	AL771310
41	9	47.4	46	17	TA114802P
42	9	47.4	46	17	TA352805Q
43	9	47.4	47	13	BJ052088
44	9	47.4	48	17	AZ831830
45	9	47.4	49	10	AW100845

ALIGNMENTS

RESULT 1
AZ606694
LOCUS IM0428D15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0428D15 R, DNA sequence.
DEFINITION
AZ606694
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 48)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Telam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0428 row: D column: 15
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 48.

FEATURES

source

1. 48
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0428D15"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

10 a 13 c 15 g

ORIGIN

Query Match 57.9%; Score 11; DB 17; Length 48;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGG 19

Db 38 ATGAACGGTGG 48

RESULT 2

AZ471573/c

LOCUS

AZ471573 19 bp DNA linear GSS 04-OCT-2000

DEFINITION

clone UUGC1M0286G13 F, DNA sequence.

ACCESSION

AZ471573.1 GI:10629698

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

FEATURES

source

1. 19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286G13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 3 c 6 g 4 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.7e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGATG 11

Db 15 CTCTAGATG 6

RESULT 3

TA116E03P

LOCUS

TA116E03P 28 bp DNA linear GSS 13-DEC-2000

DEFINITION

T. brucei sheared genomic DNA clone 116e03, forward sequence, genomic survey sequence.

ACCESSION

AL462526

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei.

ORGANISM

Trypanosoma brucei

REFERENCE

AUTHORS

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE

Direct Submission

JOURNAL

COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhle@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
Email: neilsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .28
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="116e03"

BASE COUNT 7 a 5 c 8 g 8 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 28;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAATGAACGG 16

Db 2 GAATGAACGG 11

RESULT 4

TA264G10Q 29 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 264g10, reverse sequence,
genomic survey sequence.

ACCESSION
AL487013

VERSION
AL487013.1 GI:11850630

KEYWORDS
GSS.

SOURCE
Trypanosoma brucei.

ORGANISM
Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE
1 (bases 1 to 29)

AUTHORS
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,

Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,

Meiville S.E., Rajandream M.A. and Barrell B.G.

TITLE
Direct Submission

JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: neilsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .29
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="264g10"

BASE COUNT 11 a 5 c 11 g 2 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 29;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAACG 15

Db 7 AGAATGAACG 16

RESULT 5

AV964763/c

LOCUS

DEFINITION

Intestinalis CDNA clone ciad15006 5', mRNA sequence.

ACCESSION

AV964763

VERSION

AV964763.1 GI:19454459

KEYWORDS

EST.

SOURCE

Ciona intestinalis.

ORGANISM

Ciona intestinalis

REFERENCE

1 (bases 1 to 34)

AUTHORS

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE

Expressed genes in Ciona intestinalis

JOURNAL

Unpublished (2000)

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ecid.ian.zool.kyoto-u.ac.jp.

FEATURES

source

1. .34

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="ciad15006"

/clone_lib="Nori Satoh unpublished cDNA library, young

adult"

/tissue_type="whole animal"

/dev_stage="young adult"

/notes="Vector: pBluescript SK"

BASE COUNT 12 a 5 c 8 g 9 t

ORIGIN

Query Match 52.6%; Score 10; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAT 10

Db 16 GCTCTAGAAT 7

RESULT 6

AA681423/c

LOCUS

DEFINITION

vr41f08.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone

IMAGE:1123239 5', similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A

(HUMAN); mRNA sequence.

ACCESSION

AA681423

VERSION

AA681423.1 GI:2663563

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

house mouse.

REFERENCE

1 (bases 1 to 46)

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

Unpublished (1996)

JOURNAL

Contact: Marra M/Mouse EST Project

COMMENT

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

AV964763 34 bp mRNA linear EST 14-MAR-2002
Intestinalis CDNA clone ciad15006 5', mRNA sequence.

AV964763

VERSION

AV964763.1 GI:19454459

KEYWORDS

EST.

SOURCE

Ciona intestinalis.

ORGANISM

Ciona intestinalis

REFERENCE

1 (bases 1 to 34)

AUTHORS

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE

Expressed genes in Ciona intestinalis

JOURNAL

Unpublished (2000)

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ecid.ian.zool.kyoto-u.ac.jp.

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:612575

Trace considered overall poor quality

High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1. .46
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE.1123239"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev stage="2-cell"
/lab host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified); Site 1: MluI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI (5'-CGGTGACCGTCGACCGTTTTTTTTTT-3', cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb." 13 a 19 c 7 g 7 t

BASE COUNT

13 a 19 c 7 g 7 t

Query Match 52.6%; Score 10; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGAACGGTGG 19

Db 17 TGAACGGTGG 8

RESULT 7

BH791685 49 bp DNA linear GSS 02-APR-2002
LOCUS SALK_060837.45.60.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_060837.45.60.x, DNA sequence.
ACCESSION BH791685.1 GI:19885809
VERSION BH791685
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE

1 (bases 1 to 49)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

TITLE

This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .49
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_060837.45.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines

FEATURES

Location/Qualifiers
1. .46
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE.1123239"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev stage="2-cell"
/lab host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified); Site 1: MluI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI (5'-CGGTGACCGTCGACCGTTTTTTTTTT-3', cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb." 13 a 19 c 7 g 7 t

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT

15 a 9 c 9 g 16 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAAAT 10

Db 39 GCTCTAGAAAT 48

RESULT 8

AU259636 22 bp mRNA linear EST 25-APR-2002
LOCUS AU259636 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0015510 3', mRNA sequence.
ACCESSION AU259636
VERSION AU259636.1 GI:20326342
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 22)
Kato,K. and Matoba,R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@nara.ac.jp,
URL:<http://love2.aist-nara.ac.jp/BED/index.html>.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0015510"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy" 13 a 3 c 4 g 2 t

FEATURES

Location/Qualifiers
1. .22
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0015510"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy" 13 a 3 c 4 g 2 t

BASE COUNT

13 a 3 c 4 g 2 t

ORIGIN

Query Match 47.4%; Score 9; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAAC 14

Db 11 AGAATGAAC 19

RESULT 9

AZ662500 24 bp DNA linear GSS 14-DEC-2000
LOCUS IM0541G07R Mouse 10kb plasmid UUGClM library Mus musculus genomic
DEFINITION clone UUGClM0541G07 R, DNA sequence.
ACCESSION AZ662500
VERSION AZ662500.1 GI:11799646
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 24)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

FEATURES

Location/Qualifiers
1. .49
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_060837.45.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines

BASE COUNT

13 a 3 c 4 g 2 t

ORIGIN

Query Match 47.4%; Score 9; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGAATGAAC 14

Db 11 AGAATGAAC 19

RESULT 9

AZ662500 24 bp DNA linear GSS 14-DEC-2000
LOCUS IM0541G07R Mouse 10kb plasmid UUGClM library Mus musculus genomic
DEFINITION clone UUGClM0541G07 R, DNA sequence.
ACCESSION AZ662500
VERSION AZ662500.1 GI:11799646
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 24)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
        M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
        Plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
        University of Utah Genome Center
        University of Utah
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: ddunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0541 row: G column: 07
        Seq primer: CACACGAAACACGTATGACC
        Class: plasmid ends
        High quality sequence stop: 24.
FEATURES
        source
        1. .24
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0541G07"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /notes="vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
        BASE COUNT 8 a 3 c 7 g 6 t
        ORIGIN
        Query Match 47.4%; Score 9; DB 17; Length 24;
        Best Local Similarity 100.0%; Pred. No. 1.5e+05;
        Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGAACGGTG 18
    |||||
Db 16 TGAACGGTG 24

RESULT 10
AI763346 25 bp mRNA linear EST 21-DEC-1999
LOCUS w155d06.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2394155 3'
DEFINITION similar to TR:O75053 O75053 KIAA0465 PROTEIN ;, mRNA sequence.
ACCESSION AI763346
VERSION AI763346
KEYWORDS AI763346.1 GI:5179013
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT

```

```

REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cgapsb@nci.nih.gov
        Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
        , Ph.D.
        cDNA Library Preparation: M. Bento Soares, Ph.D.
        cDNA Library Arrayed by: Greg Lennon, Ph.D.
        DNA Sequencing by: Washington University Genome Sequencing Center
        Clone distribution: NCI-CGAP clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        www.bio.llnl.gov/bbrp/image/image.html
        Insert Length: 1675 Std Error: 0.00
        Seq primer: -40UP from Gibco
        High quality sequence stop: 1.
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        1. .25
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        /db_xref="taxon:9606"
        /clone="IMAGE:2394155"
        /clone_lib="NCI CGAP Col6"
        /tissue_type="colon tumor, RER+"
        /lab_host="DH10B"
        /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
        modified polylinker; Site 1: Not 1; Site 2: Eco RI;
        Plasmid DNA from the normalized library NCI-CGAP Col6 was
        prepared, and ss circles were made in vitro. Following HAP
        purification, this DNA was used as tracer in a subtractive
        hybridization reaction. The driver was PCR-amplified cDNAs
        from a pool of 5,000 clones made from the same library
        (clones IDs 1057416-1061255, and 1144584-1145351).
        Subtraction by Bento Soares and M. Fatima Bonaldo. "
        BASE COUNT 9 a 3 c 7 g 6 t
        ORIGIN
        Query Match 47.4%; Score 9; DB 9; Length 25;
        Best Local Similarity 100.0%; Pred. No. 1.6e+05;
        Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTAGAATGA 12
    |||||
Db 12 CTAGAATGA 20

RESULT 11
AU254302/c 27 bp mRNA linear EST 25-APR-2002
LOCUS AU254302 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0001498 3', mRNA sequence.
ACCESSION AU254302
VERSION AU254302.1 GI:20315955
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL Kato,K. and Matoba,R.
COMMENT Generation of expressed sequence tags from mouse brain
        Unpublished (2002)
        Contact: Kikuya Kato
        Graduate School of Biological Sciences
        Nara Institute of Science and Technology
        8916-5 Takayama, Ikoma, Nara 630-0101, Japan
        Tel: 81-743-72-5581
        Fax: 81-743-72-5589
        Email: kkatob@bs.aist-nara.ac.jp,
        URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES
        source
        1. .27

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BASE COUNT 11 a 3 c 4 g 9 t
 ORIGIN

Query Match 47.4%; Score 9; DB 9; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAGAATGAA 13
 Db 25 TAGAATGAA 17

RESULT 12
 BH812447
 LOCUS 27 bp DNA linear GSS 02-MAY-2002
 DEFINITION SALK_061781 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_061781, DNA sequence.
 ACCESSION BH812447
 VERSION BH812447.1 GI:20390902
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 JOURNAL Arabidopsis Genome
 COMMENT Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1. .27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_061781"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 12 a 3 c 5 g 7 t
 ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAA 10
 Db 18 CTCTAGAA 26

RESULT 13
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 LOCUS 27 bp DNA linear GSS 13-JUN-2002
 DEFINITION SALK_070310.38.90.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_070310.38.90.x, DNA
 sequence.
 ACCESSION BH849811
 VERSION BH849811.1 GI:21420682
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 JOURNAL Arabidopsis Genome
 COMMENT Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1. .27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_070310.38.90.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 12 a 3 c 5 g 7 t
 ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATG 11
 Db 8 TCTAGAAATG 16

RESULT 14
 TA349B02P
 LOCUS 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 349b02, forward sequence,
 genomic survey sequence.
 ACCESSION AL493641
 VERSION AL493641.1 GI:11869420
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 TITLE Direct Submission

BASE COUNT 7 a 2 c 8 g 10 t
 ORIGIN

Query Match 47.4%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATG 11
 Db 8 TCTAGAAATG 16

RESULT 14
 TA349B02P
 LOCUS 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 349b02, forward sequence,
 genomic survey sequence.
 ACCESSION AL493641
 VERSION AL493641.1 GI:11869420
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 TITLE Direct Submission

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: neilsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

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Location/Qualifiers
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="349b02"

BASE COUNT

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAA 9

|||||
Db 7 GCTCTAGAA 15

RESULT 15

AU257604

LOCUS

AU257604 30 bp mRNA linear EST 25-APR-2002
AU257604 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0011024 3', mRNA sequence.

ACCESSION AU257604

VERSION AU257604.1 GI:20322387

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Kato, K. and Matoba, R.

Generation of expressed sequence tags from mouse brain

Unpublished (2002)

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@bs.nara.ac.jp,

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source
1. .30
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="BED0011024"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy"

13 a 6 c 4 g 7 t

BASE COUNT

ORIGIN

Query Match 47.4%; Score 9; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAA 10
|||||
Db 5 CTCTAGAA 13

Search completed: June 23, 2003, 10:10:26
Job time : 981.752 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 834.032 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table:
OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*

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- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
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- 9: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US16_NEW_COMB.seq.*
- 12: /cgn2_6/ptodata/1/pna/US17_NEW_COMB.seq.*
- 13: /cgn2_6/ptodata/1/pna/US18_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	19	100.0	21	1	PCT-US03-04088-539
C 2	19	100.0	21	1	PCT-US03-04088-543
C 3	19	100.0	21	1	PCT-US03-04088-547
C 4	19	100.0	21	1	PCT-US03-04088-551
C 5	19	100.0	21	1	PCT-US03-04088-555
C 6	19	100.0	21	1	PCT-US03-04088-559
C 7	19	100.0	23	1	PCT-US03-04088-520
C 8	19	100.0	23	1	PCT-US03-04088-521
C 9	19	100.0	26	6	US-09-721-456-598
C 10	19	100.0	26	9	US-10-325-810-598
C 11	19	100.0	26	9	US-10-359-935-23
C 12	19	100.0	30	10	US-10-330-872-5
C 13	19	100.0	30	10	US-10-330-872A-5
C 14	17	89.5	21	1	PCT-US03-04088-538
C 15	17	89.5	21	1	PCT-US03-04088-542
C 16	17	89.5	21	1	PCT-US03-04088-546
C 17	17	89.5	21	1	PCT-US03-04088-550
C 18	17	89.5	21	1	PCT-US03-04088-554
C 19	17	89.5	21	1	PCT-US03-04088-558
C 20	14	73.7	23	9	US-10-310-188-36216

21	14	73.7	24	8	US-10-442-506-39	Sequence 39, Appl
22	14	73.7	25	12	US-60-427-808-952738	Sequence 952738, A
23	14	73.7	25	13	US-60-469-545-13722	Sequence 13722, A
C 24	14	73.7	25	13	US-60-469-545-222991	Sequence 222991, A
25	13	68.4	18	6	US-09-721-456-543	Sequence 543, App
26	13	68.4	18	9	US-10-325-810-543	Sequence 543, App
C 27	13	68.4	25	6	US-09-660-222-3845	Sequence 3845, App
C 28	13	68.4	25	6	US-09-660-222-3846	Sequence 3846, App
C 29	13	68.4	25	6	US-09-660-222-3854	Sequence 3854, App
C 30	13	68.4	25	9	US-10-098-263B-118949	Sequence 118949, A
C 31	13	68.4	25	9	US-10-355-577-90268	Sequence 90268, A
C 32	13	68.4	25	9	US-10-355-577-173196	Sequence 173196, A
C 33	13	68.4	25	9	US-10-355-577-231533	Sequence 231533, A
C 34	13	68.4	25	12	US-60-427-836-69383	Sequence 69383, A
C 35	13	68.4	25	12	US-60-427-836-69383	Sequence 69383, A
C 36	13	68.4	25	12	US-60-427-836-69383	Sequence 69383, A
C 37	12	63.2	25	6	US-09-660-222-29735	Sequence 29735, A
C 38	12	63.2	25	7	US-09-954-445A-17344	Sequence 17344, A
C 39	12	63.2	25	7	US-09-954-445A-17345	Sequence 17345, A
C 40	12	63.2	25	7	US-09-954-445A-46246	Sequence 46246, A
C 41	12	63.2	25	7	US-09-954-445A-46248	Sequence 46248, A
C 42	12	63.2	25	7	US-09-954-445A-84990	Sequence 84990, A
C 43	12	63.2	25	9	US-10-098-263B-64498	Sequence 64498, A
C 44	12	63.2	25	9	US-10-355-577-2113	Sequence 2113, App
C 45	12	63.2	25	9	US-10-355-577-42242	Sequence 42242, A

ALIGNMENTS

RESULT 1

PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)-(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0%; Score 19; DB 1; Length 21;

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 GCTCTAGAAATGAACGGTGG 1

RESULT 2
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; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxybasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
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; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
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; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
PCT-US03-04088-547

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 GCTCTAGAAATGAACGGTGG 1

RESULT 4
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; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; OTHER INFORMATION: 3'-3' attached terminal deoxybasic moiety
PCT-US03-04088-543

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.1;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCUCUAGAUAAGACGGUGG 19

RESULT 3
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; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17

```

```

; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
PCT-US03-04088-551

Query Match 100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.1;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGG 19
Db 1 GCUCUAGAUGAACGGUGG 19

RESULT 5
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:

```

```
/ NAME/KEY: misc_feature
/ LOCATION: (21)..(21)
/ OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-555
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Query Match      100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATGAACGGTGG 19
    |||||
Db 19 GCTCTAGATGAACGGTGG 1
```

RESULT 6

```
PCT-US03-04088-559
; Sequence 559, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
```

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/ NAME/KEY: misc_feature
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: 2'-deoxy
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```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (1)..(1)
```

```
OTHER INFORMATION: 2'-deoxy
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (2)..(5)
```

```
OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (6)..(9)
```

```
OTHER INFORMATION: 2'-deoxy
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (10)..(10)
```

```
OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (11)..(13)
```

```
OTHER INFORMATION: 2'-deoxy
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (11)..(13)
```

```
OTHER INFORMATION: 2'-deoxy
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (11)..(13)
```

```
OTHER INFORMATION: 2'-deoxy
```

```
FEATURE:
; NAME/KEY: misc_feature
```

```
/ LOCATION: (14)..(14)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (15)..(16)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (17)..(17)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (18)..(19)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (20)..(20)
/ OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (20)..(21)
/ OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559
```

```
Query Match      100.0%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.1;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATGAACGGTGG 19
```

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|||:|||||
Db 1 GCTCTAGATGAACGGTGG 19
```

RESULT 7

```
PCT-US03-04088-520/c
; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
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```
PCT-US03-04088-520
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Query Match      100.0%; Score 19; DB 1; Length 23;
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Best Local Similarity 100.0%; Pred. No. 0.099; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 23 GCTCTAGATGAACGGTGG 5

RESULT 8
PCT-US03-04088-521/c
; Sequence 521, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; TYPE: RNA
; LENGTH: 23
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-521

Query Match 100.0%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.099; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 21 GCTCTAGATGAACGGTGG 3

RESULT 9
US-09-721-456-598
; Sequence 598, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /notes="R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-09-721-456-598

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 10
US-10-325-810-598
; Sequence 598, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

US-10-359-935-23
; Sequence 23, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Viliepointeau, Bryant
; Feng, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..26
; OTHER INFORMATION: /note= "R3c primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
US-10-325-810-598

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098; 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
RESULT 11

US-10-359-935-23
; Sequence 23, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Viliepointeau, Bryant
; Feng, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.098; 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 12
US-10-330-872-5
; Sequence 5, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C

```
; CURRENT APPLICATION NUMBER: US/10/330,872
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACGGTGG 19
Db      1 GCTCTAGAAATGAACGGTGG 19

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match      100.0%; Score 19; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGAAATGAACGGTGG 19
Db      1 GCTCTAGAAATGAACGGTGG 19

RESULT 14
PCT-US03-04088-538/c
; Sequence 538, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
```

```
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-538

Query Match      89.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 542, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
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; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 542
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-542

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Query Match      89.5%  Score 17; DB 1; Length 21;
Best Local Similarity 76.5%  Pred.No. 1.7;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 TCTAGATGAACGGTGG 19
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Search completed: June 23, 2003, 19:12:12
Job time : 834.032 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1593.58 Seconds
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299.770 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGAAATGAACGGCTGG 19

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Gapop_60.0 , Gapext 60.0

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	19	100.0	19	11	US-08-770-564A-9 Sequence 4, Appli
3	19	100.0	25	16	US-09-250-336A-4 Sequence 4, Appli
4	19	100.0	25	25	US-09-642-177-4 Sequence 27, Appli
5	19	100.0	26	1	PCT-US96-14679-27 Sequence 4, Appli
6	19	100.0	26	1	PCT-US96-14679A-27 Sequence 4, Appli
7	19	100.0	26	1	PCT-US99-03302-4 Sequence 4, Appli
8	19	100.0	26	1	PCT-US99-07533-4 Sequence 4, Appli
9	19	100.0	26	1	PCT-US99-07533-4 Sequence 23, Appli
10	19	100.0	26	6	US-08-272-102-23 Sequence 19, Appli
11	19	100.0	26	7	US-08-387-524-19 Sequence 24, Appli
12	19	100.0	26	8	US-08-472-802A-24 Sequence 24, Appli
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16	19	100.0	26	9	US-08-521-634-41 Sequence 41, Appli
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18	19	100.0	26	13	US-08-911-312-23 Sequence 23, Appli
19	19	100.0	26	13	US-08-911-312A-23 Sequence 312, App
20	19	100.0	26	13	US-08-912-951-312 Sequence 17, Appli
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Sequence 23, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 45, Appl
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Sequence 5, Appl
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Sequence 9, Appl
Sequence 26, Appl
Sequence 312, App
Sequence 312, App
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Sequence 10, Appl
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Sequence 598, App
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ALIGNMENTS

RESULT 1
PCT-US97-23619-9
; Sequence 9, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..19
OTHER INFORMATION: /note="oligo 21ab"
PCT-US97-23619-9

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
DB 1 GCTCTAGATGAACGGTGG 19

RESULT 2
US-08-770-564A-9
; Sequence 9, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-9

Query Match 100.0%; Score 19; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCTCTAGATGAACGGTGG 19

RESULT 3
US-09-250-336A-4

; Sequence 4, Application US/09250336A
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
; TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
; FILE REFERENCE: 10460-4 (210460.0004)
; CURRENT APPLICATION NUMBER: US/09/250,336A
; PRIOR FILING DATE: 1999-02-16
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1999-02-16
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4

Query Match 100.0%; Score 19; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 GCTCTAGAAATGAACGGTGG 22

RESULT 4
US-09-642-177-4
; Sequence 4, Application US/09642177
; GENERAL INFORMATION:
; APPLICANT: STROVEL, Jeffrey W.
; APPLICANT: STAMBERG, Judith
; APPLICANT: ABRUZZO, Lynne V.
; APPLICANT: HIGSHSMITH, Edward
; TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS
; TITLE OF INVENTION: 10460-4U1 (210460.0019)
; FILE REFERENCE: 10460-4U1 (210460.0019)
; CURRENT APPLICATION NUMBER: US/09/642,177
; PRIOR FILING DATE: 2000-08-18
; PRIOR FILING DATE: 1998-02-16
; PRIOR FILING DATE: 1998-02-16
; PRIOR APPLICATION NUMBER: US 60/074,793
; PRIOR FILING DATE: 1999-02-16
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/03302
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:R3c, Primer
US-09-642-177-4

Query Match 100.0%; Score 19; DB 25; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
DB 4 GCTCTAGAAATGAACGGTGG 22

RESULT 5
PCT-US96-14679-27

; Sequence 27, Application PC/TUS9614679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/14679
; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679-27

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
DB 5 GCTCTAGAAATGAACGGTGG 23

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; Sequence 27, Application PC/TUS9614679A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, BRYANT
; APPLICANT: FENG, JUNLI
; APPLICANT: ANDREWS, WILLIAM H.
; APPLICANT: ADAMS, ROBERT R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING
; TITLE OF INVENTION: TELOMERE LENGTH AND TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GERON CORPORATION
; STREET: 200 CONSTITUTION DRIVE
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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; FILING DATE: 13-SEP-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KASTER ESQ., KEVIN R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 012/045PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 473-7779
; TELEFAX: (415) 473-7750
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-14679A-27

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
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DB 5 GCTCTAGAAATGAACGGTGG 23

RESULT 7
PCT-US99-03302-4
; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamborg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward
; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; TITLE OF INVENTION: and Assessment of Disease Stage and Prognosis
; FILE REFERENCE: 1489US 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3c,
; OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||
DB 5 GCTCTAGAAATGAACGGTGG 23

RESULT 8
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; EARLIER FILING DATE: 1999-04-06

; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||
DB 5 GCTCTAGAAATGAACGGTGG 23

RESULT 9
PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||
DB 5 GCTCTAGAAATGAACGGTGG 23

RESULT 10
US-08-272-102-23
; Sequence 23, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match          100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 11
US-08-387-524-19
; Sequence 19, Application US/08387524
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,524
; FILING DATE: 13-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-387-524-19

Query Match          100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 12
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match          100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23
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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-524-19

Query Match          100.0%; Score 19; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 12
US-08-472-802A-24
; Sequence 24, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-24

Query Match          100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23
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RESULT 13
US-08-472-802B-24
; Sequence 24, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802B-24
Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
RESULT 14
US-08-482-115A-23
; Sequence 23, Application US/08482115A
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115A-23
Query Match 100.0%; Score 19; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23
RESULT 15
US-08-520-550-19
; Sequence 19, Application US/08520550
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-520-550-19

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Query Match      100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGATGAACGGTGG 19
Db      5 GCTCTAGATGAACGGTGG 23

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Job time : 1593.65 secs

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OM nucleic - nucleic search, using sw model

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Title: US-08-770-564A-9

Perfect score: 19
Sequence: 1 GCTCTAGATGACGGTGG 19

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Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	100.0	26	9	US-10-044-539-312
3	19	100.0	26	10	US-09-057-351-23
4	13	68.4	25	9	US-10-098-263B-118949
5	13	68.4	26	9	US-09-352-522B-19
6	13	68.4	28	10	US-09-844-006A-3
7	12	63.2	23	9	US-09-952-522B-17
8	12	63.2	23	9	US-09-952-522B-31
9	12	63.2	25	9	US-10-215-112-6862
10	12	63.2	25	9	US-10-098-263B-64498
11	12	63.2	26	9	US-10-011-366-16
12	11	57.9	17	10	US-09-969-373-1959
13	11	57.9	21	9	US-09-997-868-13
14	11	57.9	22	10	US-09-765-873A-5
15	11	57.9	23	9	US-09-952-522B-9
16	11	57.9	24	9	US-09-754-853A-676
17	11	57.9	24	9	US-10-245-813-2
18	11	57.9	25	9	US-10-098-263B-10750
19	11	57.9	25	9	US-10-098-263B-22667

ALIGNMENTS

RESULT 1

US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 2
US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 19; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 3
US-09-057-351-23
Sequence 23, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Villegonteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 19; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 4

US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118949

Query Match 68.4%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATGAACG 15
|||||
Db 20 TCTAGAAATGAACG 8

RESULT 5

US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer

US-09-952-522B-19

Query Match 68.4%; Score 13; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
|||||
Db 1 GCTCTAGAAATGAA 13

RESULT 6

US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match 68.4%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
|||||
Db 1 GCTCTAGAAATGAA 13

RESULT 7

US-09-952-522B-17
; Sequence 17, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 23

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
; OTHER INFORMATION: forward primer
US-09-952-522B-17

Query Match      63.2%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
   |||||
Db 1 GCTCTAGATGA 12

RESULT 8
US-09-952-522B-31
; Sequence 31, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Llull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
; OTHER INFORMATION: forward primer
US-09-952-522B-31

Query Match      63.2%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
   |||||
Db 1 GCTCTAGATGA 12

RESULT 9
US-10-215-112-6862/c
; Sequence 6862, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6862
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6862

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
   |||||
Db 15 GCTCTAGATGA 4

RESULT 10
US-10-098-263B-64498/c
; Sequence 64498, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64498
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64498

Query Match      63.2%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAAC 14
   |||||
Db 23 TCTAGATGAAC 12

RESULT 11
US-10-011-366-16
; Sequence 16, Application US/10011366
; Publication No. US20030054493A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Kink, John A.
; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
DISEASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,366
; FILING DATE: 16-Nov. US20030054493A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,310
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;; FILING DATE: 23-OCT-1997
;; APPLICATION NUMBER: US 08/329,154
;; FILING DATE: 24-OCT-1994
;; APPLICATION NUMBER: US 08/161,907
;; FILING DATE: 02-DEC-1993
;; APPLICATION NUMBER: US 07/985,321
;; FILING DATE: 04-DEC-1992
;; APPLICATION NUMBER: US 07/429,791
;; FILING DATE: 31-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: OPND-01121
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16

Query Match 63.2%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGA 12
DB 1 GCTCTAGATGA 12

RESULT 12

US-09-969-373-1959
;; Sequence 1959, Application US/09969373
;; Patent No. US20020133852A1
;; GENERAL INFORMATION:
;; APPLICANT: Effertz, Roger J.
;; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;; FILE REFERENCE: 38-10(S2679)A
;; CURRENT APPLICATION NUMBER: US/09/969,373
;; CURRENT FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US 09/754,853
;; PRIOR FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 09/760,427
;; PRIOR FILING DATE: 2001-01-13
;; PRIOR APPLICATION NUMBER: US 09/855,768
;; PRIOR FILING DATE: 2001-05-15
;; NUMBER OF SEQ ID NOS: 4593
;; SEQ ID NO 1959
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Glycine max
US-09-969-373-1959

Query Match 57.9%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ATGAACGGTGG 19
DB 6 ATGAACGGTGG 16

RESULT 13

US-09-997-868-13/c
;; Sequence 13, Application US/09997868
;; Publication No. US20030031654A1
;; GENERAL INFORMATION:

;; APPLICANT: Gorman, Cornelia M.,
;; Groskreutz, Debyra J.
;; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
;; Polypeptide Synthesis
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA: US/09/997,868
;; FILING DATE: 12-Mar-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/887265
;; FILING DATE: 22-MAY-1992
;; APPLICATION NUMBER: 07/803631
;; FILING DATE: 06-DEC-1992
;; APPLICATION NUMBER: PCT/US92/10621
;; FILING DATE: 04-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P0748P3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match 57.9%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 11 GCTCTAGATG 1

RESULT 14

US-09-765-873A-5
;; Sequence 5, Application US/09765873A
;; Patent No. US20010053847A1
;; GENERAL INFORMATION:
;; APPLICANT: Tang, Xiao-Song
;; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
;; FILE REFERENCE: BC1009 US CIP
;; CURRENT APPLICATION NUMBER: US/09/765,873A
;; CURRENT FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: US 09/627,216
;; PRIOR FILING DATE: 2000-07-27
;; PRIOR APPLICATION NUMBER: US 60/147,719
;; PRIOR FILING DATE: 1999-08-06
;; NUMBER OF SEQ ID NOS: 38
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 5
;; LENGTH: 22
;; TYPE: DNA
;; ORGANISM: primer

US-09-765-873A-5

Query Match 57.9% Score 11; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
| | | | | | | | | |
Db 3 GCTCTAGATG 13

RESULT 15

US-09-952-522B-9
; Sequence 9, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Lluall, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: osteocalcin forward primer
US-09-952-522B-9

Query Match 57.9% Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
| | | | | | | | | |
Db 1 GCTCTAGATG 11

Search completed: June 23, 2003, 20:01:32
Job time : 152.681 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 29.749 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: us-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGATGAACGGTGG 19

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	2 US-08-770-565-9	Sequence 9, Appli
2	19	100.0	26	1 US-08-330-123A-23	Sequence 23, Appl
3	19	100.0	26	1 US-08-482-115B-23	Sequence 23, Appl
4	19	100.0	26	2 US-08-660-678A-23	Sequence 23, Appl
5	19	100.0	26	2 US-08-710-249-26	Sequence 26, Appl
6	19	100.0	26	2 US-08-485-778-19	Sequence 19, Appl
7	19	100.0	26	2 US-08-472-802C-24	Sequence 24, Appl
8	19	100.0	26	3 US-08-520-550A-19	Sequence 19, Appl
9	19	100.0	26	3 US-08-598-443-23	Sequence 23, Appl
10	19	100.0	26	4 US-08-974-549A-598	Sequence 598, App
11	19	100.0	26	4 US-09-060-523-23	Sequence 23, Appl
12	19	100.0	26	4 US-09-220-157A-26	Sequence 26, Appl
13	19	100.0	26	4 US-09-286-959B-4	Sequence 4, Appli
14	19	100.0	26	4 US-08-580-517-23	Sequence 23, Appl
15	19	100.0	27	2 US-08-770-565-26	Sequence 26, Appl
16	19	100.0	30	2 US-08-770-565-8	Sequence 8, Appli
17	18	94.7	30	2 US-08-833-377-6	Sequence 6, Appli
18	15	78.9	15	2 US-08-770-565-10	Sequence 10, Appl
19	14	73.7	27	3 US-08-630-172-24	Sequence 24, Appl
20	14	73.7	27	4 US-09-375-419-24	Sequence 24, Appl
21	13	68.4	18	4 US-08-974-549A-543	Sequence 543, App
22	12	63.2	26	1 US-08-480-604A-16	Sequence 16, Appl
23	12	63.2	26	2 US-08-405-496A-16	Sequence 16, Appl
24	12	63.2	26	4 US-08-915-136-16	Sequence 16, Appl
25	12	63.2	26	4 US-08-957-310-16	Sequence 16, Appl
26	12	63.2	30	1 US-08-349-006-3	Sequence 3, Appli
27	12	63.2	30	5 PCT-US94-02107-3	Sequence 3, Appli

28 12 63.2 33 3 US-08-630-172-22 Sequence 22, Appl
29 12 63.2 33 4 US-09-375-419-22 Sequence 22, Appl
30 11 57.9 11 2 US-08-770-565-11 Sequence 11, Appl
C 31 11 57.9 21 4 US-08-026-143B-13 Sequence 13, Appl
C 32 11 57.9 21 5 PCT-US92-10621-13 Sequence 13, Appl
33 11 57.9 21 5 PCT-US94-02233-13 Sequence 13, Appl
34 11 57.9 22 4 US-09-627-216A-5 Sequence 5, Appl
35 11 57.9 23 3 US-08-973-068-46 Sequence 46, Appl
36 11 57.9 26 4 US-09-153-310-4 Sequence 4, Appl
37 11 57.9 30 2 US-08-995-927-7 Sequence 7, Appl
38 11 57.9 30 4 US-09-349-627-5 Sequence 5, Appl
39 11 57.9 30 4 US-09-582-096-7 Sequence 7, Appl
40 11 57.9 37 1 US-08-591-492-17 Sequence 17, Appl
41 11 57.9 37 3 US-08-815-190A-3 Sequence 3, Appl
42 11 57.9 39 4 US-09-091-305-3 Sequence 3, Appl
43 11 57.9 40 1 US-08-395-800A-12 Sequence 12, Appl
C 44 11 57.9 46 1 US-08-399-696-14 Sequence 14, Appl
45 11 57.9 50 1 US-08-374-641-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19

Db 1 GCTCTAGATGAACGGTGG 19
|||||

RESULT 2

US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
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Db 5 GCTCTAGATGAACGGTGG 23

RESULT 3

US-08-482-115B-23
; Sequence 23, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 100.0%; Score 19; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||

Db 5 GCTCTAGATGAACGGTGG 23

RESULT 4

US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 5
US-08-710-249-26
Sequence 26, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
DB 5 GCTCTAGATGAACGGTGG 23

RESULT 6
US-08-485-778-19
Sequence 19, Application US/08485778
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel Athena
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 7
US-08-472-802C-24
; Sequence 24, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 100.0%; Score 19; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 8
US-08-520-550A-19
; Sequence 19, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol

; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-520-550A-19

Query Match 100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
|||||
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 9
US-08-998-443-23
; Sequence 23, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US/08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-23

Query Match 100.0%; Score 19; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 10
US-08-974-549A-598
Sequence 598, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
```


ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-580-517-23

Query Match 100.0%; Score 19; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 15
US-08-770-565-26
Sequence 26, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0023000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-26

Query Match 100.0%; Score 19; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

Search completed: June 23, 2003, 10:17:07
Job time : 30.749 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 126.263 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-9

Perfect score: 19

Sequence: 1 GCTCTAGATGACGGTGG 19

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	AAV41176	RNA component of h
2	19	100.0	25	AAZ08704	Human telomerase R
3	19	100.0	26	AAT10304	RNA component of h
4	19	100.0	26	AAT10299	RNA component of h
5	19	100.0	26	AAT11044	Primer for product
6	19	100.0	26	AAT58811	Human telomerase P
7	19	100.0	26	AAV19489	Human htr gene R
8	19	100.0	26	AAV17033	Telomerase PCR pri
9	19	100.0	26	AAZ90788	Human telomerase R

10	19	100.0	26	20	AAZ77402	Human telomerase R
11	19	100.0	26	20	AAZ01542	PCR primer for Hum
12	19	100.0	26	21	AAA88250	Human telomerase R
13	19	100.0	26	24	ABK48024	Human telomerase-a
14	19	100.0	26	24	ABK24246	Human telomerase (
15	19	100.0	27	19	AAV41193	RNA component of h
16	19	100.0	27	24	ABA95497	Human telomerase R
17	19	100.0	30	19	AAV63649	Antisense oligonuc
18	19	100.0	30	19	AAV41175	RNA component of h
19	19	100.0	30	20	AAZ23631	Human clone 28-1 t
20	19	100.0	30	22	AAZ09476	Antisense oligonuc
21	19	100.0	30	23	AAZ15928	Human telomerase p
22	19	100.0	30	24	ABA91517	Oligonucleotide us
23	15	78.9	15	19	AAV41177	RNA component of h
24	14	73.7	15	23	AAZ15931	Human telomerase p
25	14	73.7	27	18	AAT97049	Sense primer for h
26	13	68.4	13	23	AAZ15930	Human telomerase p
27	13	68.4	28	24	ABA04366	CRT C-domain-green
28	13	68.4	32	21	AAZ46113	Human GPCR TDAG8(I
29	12	63.2	17	22	AAF57369	Murine Cdc25A intr
30	12	63.2	26	17	AAT29258	C. difficile toxin
31	12	63.2	26	19	AAZ30567	Clostridium diffic
32	12	63.2	26	21	ABK09963	Novel recombinant
33	12	63.2	30	15	AAQ71630	HCWV IR-exon-4 sub
34	12	63.2	33	18	AAT97047	Sense primer for h
35	12	63.2	39	22	AAF81502	Novel human G prot
36	12	63.2	39	22	AAF87602	DNA associated wit
37	11	57.9	11	19	AAV41178	RNA component of h
38	11	57.9	11	23	AAZ15929	Human telomerase p
39	11	57.9	15	23	AAZ15932	Human telomerase p
40	11	57.9	19	22	AAH43421	ISA3 reverse prime
41	11	57.9	21	14	AAQ43258	Sequence encoding
42	11	57.9	21	14	AAQ43257	Sequence encoding
43	11	57.9	21	15	AAQ71457	Rx'2.4 proroelaxin
44	11	57.9	22	24	AAZ33073	Phenylalanine ammo
45	11	57.9	22	24	AAZ26921	Rhodospiridium tor

ALIGNMENTS

RESULT 1
AAV41176
ID AAV41176 standard; DNA; 19 BP.
XX
AC AAV41176;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (htr) antisense oligo 21ab.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraction; sterility; immunosuppression; therapeutic; htr;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
DR

XX New polynucleotide(s) anti-sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AA41169 to AA41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridize to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridize to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence: 19 BP; 5 A; 3 C; 7 G; 4 T; 0 other;
XX
XX Query Match 100.0%; Score 19; DB 19; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 0.042;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTCTAGATGAACGGTGG 19
XX |||||
XX Db 1 GCTCTAGATGAACGGTGG 19
XX
XX RESULT 2
XX AAZ08704
XX ID AAZ08704 standard; DNA; 25 BP.
XX AC AAZ08704;
XX
XX DT 20-OCT-1999 (first entry)
XX
XX DE Human telomerase RNA template PCR primer R3C.
XX
XX KW Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
XX KW telomeric repeat amplification protocol; detection; PCR primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9941406-A1.
XX
XX PD 19-AUG-1999.
XX
XX PF 16-FEB-1999; 99WO-US03302.
XX
XX PR 16-FEB-1998; 98US-0074793.
XX
XX (UTMA-) UNIV MARYLAND BALTIMORE.
XX
XX PI Abruzzo LV, Highsmith E, Stamberg J, Strovel JW;
XX WPI; 1999-508655/42.
XX
XX DR Detecting telomerase activity in non-cellular body fluid using a
XX PT modified telomeric repeat amplification protocol
XX

PS Disclosure; Page 16; 32pp; English.
XX
XX A method has been developed for detecting telomerase activity in a
CC non-cellular portion of body fluid from a cancer patient using a
CC modified telomeric repeat amplification protocol (TRAP). A method for
CC detecting cancer comprises: (a) removing the cellular portion of a body
CC fluid specimen from the patient; (b) preparing a protein extract from
CC the body fluid remainder; (c) assaying the extract for the presence and
CC quantity of telomerase RNA or telomerase activity; and (d) comparing the
CC results with normal levels, to determine the presence of cancer. The
CC methods are used in cancer diagnosis and prognosis, and also to monitor
CC cancer therapy effectiveness. Unlike prior art telomerase activity
CC assays in cancer patients, the method allows noninvasive sample
CC collection. The methods are also more reliable and less tumour specific
CC than other methods which detect circulating tumour markers. The present
CC sequence represents a human telomerase RNA template PCR primer used in
CC the exemplification of the present invention.
XX
XX Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;
XX
XX Query Match 100.0%; Score 19; DB 20; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 0.041;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTCTAGATGAACGGTGG 19
XX |||||
XX Db 4 GCTCTAGATGAACGGTGG 22
XX
XX RESULT 3
XX AAT10304
XX ID AAT10304 standard; DNA; 26 BP.
XX AC AAT10304;
XX
XX DT 10-SEP-1996 (first entry)
XX
XX DE RNA component of human telomerase nested PCR primer R3c.
XX
XX KW RNA component; human; telomerase; polymerase chain reaction;
XX KW recombinant production; synthesis; mutant; detection; mammalian;
XX KW identification; modulating agent; neoplastic condition;
XX KW transcriptional regulatory sequence; gene therapy; disease;
XX KW PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO9601835-A1.
XX
XX PD 25-JAN-1996.
XX
XX PF 06-JUL-1995; 95WO-US08530.
XX
XX PR 07-JUN-1995; 95US-0482115.
XX PR 07-JUL-1994; 94US-0272102.
XX PR 27-OCT-1994; 94US-0330123.
XX PR 07-JUN-1995; 95US-0472802.
XX
XX (GERO-) GERON CORP.
XX
XX PI Andrews WH, Feng J, Funk W, Villeponteau B;
XX WPI; 1996-097581/10.
XX
XX DR RNA component of mammalian telomerase, esp. human - useful in
XX PT identifying e.g. candidate telomerase-modulating agents
XX
XX PS Example 10; Page 82; 114pp; English.
XX
XX The present sequence, a nested PCR primer for the RNA component
CC of human telomerase (RCHT), was used in a 5' RACE procedure. The
CC RCHT can be used in the recombinant prodn. of an active telomerase
CC mol., capable of adding sequences to chromosomal DNA telomeres, and

CC	therapy of human diseases.
xx	
sq	Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
	Query Match 100.0%; Score 19; DB 17; Length 26;
	Best Local Similarity 100.0%; Pred. No. 0.041;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

DD 3 GCCTCAGAAATGACCGG1G
 RESULT 5
 AAT11044
 ID AAT11044 standard: DNA: 25 bp.

AAT11044
 ID AAT11044 standard; DNA; 26 BP.
 XX
 AC AAT11044:

DI
02-JUL-1996 (first entry)
XX

Primer for production of telomerase antisense oligonucleotide:

Telomerase; mammal; antisense; triplex forming oligonucleotide;
KW
KW
Telomerase; mammal; probe; primer; ribozyme; ss.
plasmid; KW

XX
OS
Synthetic.

XX PN WO9601614-A2.

XX	25-JAN-1996.
PD	
XX	
PF	07-JUL-1995; 95WO-US08620.
XX	
PR	07-JUN-1995; 95US-0485778.

PR 27-OCT-1999

PK
XX
13-FEB-1993; 9303-038/324.

PA (COLD-) COLD SPRING
PA (GERO-) GERON CORP.

PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;

XX
FI MAIUSCULA PA, VILTERPONTA PA,

DK XX
REF; 1338-03/428/10.

PT RNA components of (non)human studying cell senescence and

XX
XX
XXXXXXX Error!XX
Example 8, page 22, odd, right.

CC The RNA components
CC from mouse, rat and
CC

telomerase; probes and primers can be used in detection; vectors
host cells transformed with the isolated telomerase genes can be

CC used for production of telomerases
CC forming oligonucleotides directed

be used therapeutically as can plasmids. A mouse which lacks the telomerase gene (also claimed) can be used for study of telomere regulation in vivo, and the role it plays in immortalisation. Three primers (AAT11040, AAT11043, AAT11044) were used to produce antisense oligonucleotides which were then used to produce antisense expression plasmids. AAT11040 was used alongside both AAT11043 and AAT11044 to produce two different antisense molecules.

Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other; SQ

Query Match
100.0%; Score 19; DB 17; Length 26;

Best local similarity 100.0%, freq. NO: 0.041,
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 6

AAAT58811
 ID AAT58811 standard; DNA; 26 BP.
 AC AAT58811;
 XX
 XX
 DT 20-NOV-1997 (first entry)
 XX
 XX Human telomerase PCR 3'-primer R3C.

XX Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
 KW protozoa; tumour; antibody; polymerase chain reaction; ss.
 XX

OS Synthetic.

XX WO9640868-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09517.

XX 07-JUN-1995; 95US-0478352.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Autexier C, Greider C;

XX WPI; 1997-099928/09.

XX DNA encoding essential RNA components of human telomerase - also
 PT truncated or recombinant telomerase, useful for diagnosis and
 PT treatment of cancer and infection by eukaryotic parasites

XX Example 5; Page 32; 48pp; English.

XX The present sequence represents PCR 3'-primer R3C used for
 CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
 CC hybridisation assays to detect or quantify telomerase activity in cells,
 CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
 CC (yeast and protozoa) or tumours. It is also useful as primers for
 CC amplification assays. The truncated or recombinant vertebrate telomerase
 CC is used therapeutically to increase telomerase activity (also as
 CC reagents in the screening assay) while the RNA or other inhibitors such
 CC as antisense molecules, are used to reduce such activity. Typical
 CC applications are initiation/restoration of activity to cause senescence
 CC or to prevent immortalisation of cells in tumours or parasites. The DNA
 CC is also used to produce recombinant telomerase, which can then be used
 CC conventionally to raise antibodies for diagnostic detection of
 CC telomerase. Detecting telomerase allows early diagnosis of tumour or
 CC infection, before clinical signs manifest. Telomerase inhibitors
 CC directed against e.g. Trypanosoma should cause fewer side effects than
 CC drugs currently used to treat such infections. The DNA encodes those
 CC parts of hTR RNA essential for activity but are significantly shorter
 CC than the endogenous RNA component.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 18; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 7

AAV19489

ID AAV19489 standard; DNA; 26 BP.
 XX
 AC AAV19489;
 XX
 XX
 DT 28-AUG-1998 (first entry)
 XX
 XX Human hTR gene RT-PCR primer R3c.
 DE
 XX hTR gene; TPC2; TPC3; telomere length; telomerase; human; cancer;
 KW gene therapy; diagnosis; PCR; primer; ss.
 XX

OS Synthetic.

OS Homo sapiens.

XX WO9811204-A1.

XX 19-MAR-1998.

XX 13-SEP-1996; 96WO-US14679.

XX 13-SEP-1996; 96WO-US14679.

XX (GERO-) GERON CORP.

XX Adams RR, Andrews WH, Feng J, Villeponteau B;

XX WPI; 1998-207373/18.

XX Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
 PT telomerase activity

XX Disclosure; Page 49; 86pp; English.

XX Primers R3c and F3b (see AAV19488) were designed for the PCR
 CC amplification of the human telomerase hTR gene (see AAV19481). hTR
 CC mRNA levels were showed to correlate with telomerase activity
 CC levels in a variety of mortal and immortal cell lines. Methods of
 CC the invention allow detection and quantitation of TPC2 (see
 CC AAV19479), TPC3 (see AAV19480) and/or TPC2 gene products and can be
 CC used to detect immortal cells, especially telomerase positive
 CC cancer cells.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23

RESULT 8

AAV17033

ID AAV17033 standard; DNA; 26 BP.

XX AAV17033;

XX 13-AUG-1998 (first entry)

XX Telomerase PCR primer R3c.

XX Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
 KW PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.
 XX 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 XX WPI; 1998-171633/16.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX
 PS Example 2; Page 218; 387pp; English.
 XX
 CC The present sequence represents a PCR primer from the present invention
 CC which describes human telomerase reverse transcriptase (hTERT). The
 CC present invention also describes the following methods: (A) determining
 CC whether a test compound is a modulator of hTERT, by detecting the change
 CC in hTERT recombinant protein or polynucleotide, on administration of the
 CC compound; (B) preparation of recombinant telomerase by contacting a
 CC protein preparation of hTERT with a telomerase RNA component; (C)
 CC detection of the hTERT RNA or protein in a sample by binding a relevant
 CC probe to the sample and detecting the complex formed or in the case of
 CC RNA detection, amplifying the product and correlating the presence of
 CC complex or amplification product with presence of hTERT in the sample;
 CC and (D) increasing the proliferation of a vertebrate cell by increasing
 CC hTERT expression; and (E) the use of an agent that causes an increase in
 CC cell vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 19; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGG 19
 Db 5 GCTCTAGATGAACGGTGG 23
 RESULT 9
 AAX90788
 ID AAX90788 standard; DNA; 26 BP.
 AC
 XX AAX90788;
 XX
 DT 13-JAN-2000 (first entry)
 XX
 DE Human telomerase RNA specific PCR primer-2.
 XX
 KW PCR primer; human telomerase RNA; hTR; amplify; human staufen cDNA;
 KW hStau; synthesised; random hexamer primer;
 KW Superscript II reverse transcriptase; ss.
 XX
 OS Synthetic.

OS Homo sapiens.
 XX
 PN WO9951255-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 06-APR-1999; 99WO-US07533.
 XX
 PR 06-APR-1998; 98US-0080783.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 XX Greider CW, Le S;
 XX
 XX WPI; 1999-620168/53.
 XX
 PT Human staufen polypeptide useful in methods for identifying telomerase
 PT inhibitors -
 XX
 PS Disclosure; Page 15; 50pp; English.
 XX
 CC The present sequence is a PCR primer specific to human telomerase
 CC RNA (hTR). It is used to amplify human staufen (hStau) cDNA synthesised
 CC using random hexamer primers and Superscript II reverse transcriptase.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 100.0%; Score 19; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGG 19
 Db 5 GCTCTAGATGAACGGTGG 23
 RESULT 10
 AAX77402
 ID AAX77402 standard; DNA; 26 BP.
 XX
 AC AAX77402;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE Human telomerase RNA PCR primer TE-hTR3.1.
 XX
 KW Telomerase; human; diagnosis; bladder cancer; detection; urine;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN EP926245-A2.
 XX
 XX 30-JUN-1999.
 XX
 XX 21-DEC-1998; 98EP-0124326.
 XX
 XX 22-DEC-1997; 97DE-1057300.
 XX
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 XX Emrich T;
 XX
 XX WPI; 1999-349242/30.
 XX
 XX Detecting telomerase RNA in urine - useful for diagnosis of bladder
 XX cancer
 PT
 XX
 XX Claim 6; Page 10; 13pp; German.
 XX
 XX This invention describes a novel method for diagnosing bladder cancer
 XX which comprises detecting telomerase RNA in a urine sample. The method

CC of the invention has greater sensitivity and reliability than assays for
 CC telomerase activity (cf. WO 9735871). This sequence represents a primer
 CC used in the method of the invention.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11

AAK01542

ID AAX01542 standard; DNA; 26 BP.

XX AC

XX AAX01542;

XX 29-APR-1999 (first entry)

XX DE

XX PCR primer for Human TPC3 gene.

XX TPC2; TPC3; human; telomere length regulation; cancer; pregnancy;

XX fertility; diagnosis; therapy; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN

XX US5858777-A.

XX PD

XX 12-JAN-1999.

XX PF

XX 13-SEP-1996; 96US-0710249.

XX PR

XX 08-SEP-1995; 95US-0003492.

XX PR

XX 05-JAN-1996; 96US-0583808.

XX PR

XX 13-SEP-1996; 96US-0710249.

XX PA

XX (GERO-) GERON CORP.

XX PI

XX Adams RR, Andrews WH, Feng J, Villeponteau B;

XX DR

XX WPI; 1999-152104/13.

XX XX

XX DNA encoding proteins TPC2 and TPC3 - useful for regulating telomere

XX length or modulating telomerase activity

XX PS

XX Example; Column 38; 59pp; English.

XX CC

XX This sequence represents a PCR primer for DNA encoding the human TPC3

XX protein, which is contained within the recombinant mammalian host cell of

XX the invention. The invention provides methods and reagents for regulating

XX telomere length and modulating telomerase activity in mammalian cells as

XX well as for detecting, diagnosing, and treating related diseases and

XX conditions such as cancer, pregnancy, or fertility in humans and other

XX mammals.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

Db 5 GCTCTAGATGAACGGTGG 23

RESULT 12

AAA88250

ID AAA88250 standard; DNA; 26 BP.

XX AC

XX AAA88250;

XX DT 15-DEC-2000 (first entry)

XX DE Human telomerase RNA reverse transcriptase PCR primer #2.

XX KW Human; telomerase; hTR; reverse transcriptase; RT-PCR; PCR primer;

XX KW detection; cancer; micrometastasis; diagnosis; ss.

XX OS Homo sapiens.

XX PN WO200046601-A1.

XX PD 10-AUG-2000.

XX PF 01-FEB-2000; 2000WO-IB00100.

XX PR 02-FEB-1999; 99GB-0002302.

XX PA (LABS/) LARSEN F.

XX PA (SKAA/) SKAANSENG M.

XX PI Larsen F, Skaanseng M;

XX DR WPI; 2000-491281/43.

XX XX

XX Detecting telomerase activity in samples, useful for diagnosis of

XX cancer and micrometastasis, comprises treating sample with solid phase,

XX PT removing solid phase and treating to elute bound telomerase

XX Example 11; Page 38; 68pp; English.

XX CC

XX The present invention describes a method (I) for detecting telomerase

XX activity in a sample. The method comprises treating the sample with a

XX solid phase to bind telomerase, separating the solid phase from the

XX sample to form a test sample which may be treated to elute bound

XX telomerase and assaying the sample for telomerase activity. Also

XX described are: (i) a kit (ii) for detecting telomerase activity,

XX comprising a solid phase and one or more components for assaying

XX telomerase activity; and (2) a component (iii) of an assay system for

XX detecting telomerase activity, comprising a solid phase for binding

XX telomerase on which is present a substrate for telomerase elongation.

XX (i) is useful for cancer diagnosis or prognosis and detection of

XX micrometastasis as detection of telomerase activity is indicative of

XX cancer or micrometastasis. The solid phase used in (i) is useful for

XX separating telomerase from a sample and therefore for detecting

XX telomerase activity. (ii) is useful for detection of cancer cells and

XX may also comprise means for assaying an mRNA diagnostic for cancer.

XX The present sequence represents a reverse transcriptase (RT) PCR primer

XX for human telomerase RNA, which is used in an example from the present

XX invention.

XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

Db 5 GCTCTAGATGAACGGTGG 23

RESULT 13

ABK48024

ID ABK48024 standard; DNA; 26 BP.

XX AC

XX ABK48024;

XX DT 18-JUN-2002 (first entry)

XX XX

DE Human telomerase-associated RNA template (hTR), PCR primer hTR2.
XX Human; telomerase-associated RNA template; hTR; endometrial;
KW malignancy; cancer; breast; ovarian; head and neck; lung; cervical;
KW colorectal; gastric; liver; pancreatic; bladder; prostate;
KW brain; kidney; oesophagus; melanoma; sarcoma; premalignancy;
KW carcinoma in-situ; cervical dysplasia; bronchial dysplasia;
KW cervical intraepithelial neoplasia; atypical hyperplasia;
KW colorectal adenoma; atypical endometrial hyperplasia; tumour;
KW Barrett's oesophagus; telomerase-directed therapy; primer; ss.
XX Homo sapiens.
OS
XX
XX WO200218652-A2.
PN
XX
XX
PD 07-MAR-2002.
XX
XX 28-AUG-2001; 2001WO-US26749.
PF
XX 31-AUG-2000; 2000US-0653573.
PR
XX (ONCO-) ONCOMEDX INC.
PA
XX Kopseski MS; Gocke CD;
PI
XX
XX WPI; 2002-269532/31.
DR
XX
XX
PT Detecting human telomerase RNA template RNA or human telomerase reverse
PT transcriptase protein RNA in bodily fluid, useful as marker for
PT diagnosing, monitoring or treating cancer, carcinoma in situ or
PT premalignancy -
XX
XX Example 1; Page 14; 30pp; English.
XX
XX The invention relates to detecting human telomerase RNA template (hTR)
CC RNA or human telomerase reverse transcriptase protein RNA (hTRT) RNA (I)
CC in a bodily fluid, comprising amplifying RNA extracted from plasma or
CC serum sample, or its corresponding cDNA comprising (I), using primers or
CC probes that target (I) or cDNA and detecting qualitatively or
CC quantitatively amplified product of (I) or cDNA product. The method is
CC useful for detecting (I) in a bodily fluid, which is useful for
CC identifying a human having (I) expressing cells or tissue which
CC include a malignancy preferably a cancer of breast, ovarian, head and
CC neck, lung, cervical, colorectal, gastric, liver, pancreatic, bladder,
CC prostate, endometrial, brain, kidney, or oesophagus, or a melanoma or
CC sarcoma, premalignancy or carcinoma in-situ, preferably cervical
CC dysplasia, cervical intraepithelial neoplasia, bronchial dysplasia,
CC atypical hyperplasia of the breast, ductal carcinoma in-situ,
CC colorectal adenoma, atypical endometrial hyperplasia, or Barrett's
CC oesophagus, where the human is at risk for developing a malignancy or
CC premalignancy or is known to have malignancy, premalignancy or
CC carcinoma in situ. The method is also useful for treating a human with
CC cancer for telomerase-directed therapy, which comprises selecting the
CC human for the therapy after detection of (I), for determining a
CC need for diagnostic test in a human with malignancy or premalignancy
CC and for monitoring a therapy administered to a human. (I) provides a
CC marker which is utilised as a guide to whether adequate therapeutic
CC effect has been achieved, or whether additional or more advanced therapy
CC is required, and to assess prognosis in these patients. The method also
CC allows identification or analysis, either quantitatively or
CC qualitatively, of (I) in plasma or serum of humans during or following
CC surgical procedures to remove premalignant or malignant lesions, and thus
CC allow stratification of such patients as to their risk of residual
CC cancer following surgery, and their need for further therapy or who has
CC completed therapy as an early indicator or relapsed cancer, impending
CC relapse, or treatment failure. The method allows the development and
CC application of telomerase-specific therapy even when only premalignant
CC tumours, early cancer, or occult cancer or metastasis such as following
CC resection or in minimal residual disease are present. The present
CC sequence represents a PCR primer for human telomerase-associated
CC RNA template (hTR).
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 19; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
|||||
DB 5 GCTCTAGATGAACGGTGG 23
|||||
RESULT 14
AAD24246
ID AAD24246 standard; DNA; 26 BP.
XX
XX AAD24246;
XX
XX 07-MAR-2002 (first entry)
XX
XX Human telomerase (hTR) cDNA amplifying R3c downstream RT-PCR primer.
XX Human; telomerase; TR; telomerase activity-related disease; therapy;
KW cancer; pregnancy; fertility; RT-PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6300110-B1.
XX
XX 09-OCT-2001.
XX
XX 23-DEC-1998; 98US-0220157.
XX
XX 09-SEP-1995; 95US-003492P.
PR 13-SEP-1996; 96US-0710249.
PR 05-JAN-1996; 96US-0583808.
XX
XX (GERO-) GERON CORP.
XX
XX Villeponteau B, Feng J, Andrews WH, Adams RR;
PI WPI; 2002-033174/04.
DR
XX Peptide products of the human TPC2 and TPC3 gene are involved in
PT regulation of telomere length and activity are useful to diagnose and
PT treat telomere length and activity-related diseases -
XX
XX Example; Column 38; 60pp; English.
XX
XX The invention relates to methods and reagents for regulating telomere
CC length and for modulating telomerase activity in mammalian cells. The
CC invention also relates to purified, synthetic or recombinant peptides
CC such as TPC2 or TPC3 used for detecting regulators of telomere length
CC and telomerase activity in mammalian cells and for a variety of related
CC diagnostic and therapeutic purposes. The method is useful for screening,
CC diagnosing, monitoring and treating diseases and other conditions such as
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC The present sequence is a reverse transcription (RT) PCR primer
CC used for amplifying human telomerase (hTR) cDNA.
XX
XX Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 19; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACGGTGG 19
|||||
DB 5 GCTCTAGATGAACGGTGG 23
|||||
RESULT 15
AAV41193
ID AAV41193 standard; DNA; 27 BP.
XX

AC AAV41193;
 XX
 DT 08-OCT-1998 (first entry)
 XX
 DE RNA component of human telomerase (hTR) amplifying reverse primer.
 XX
 KW RNA component; human telomerase; antisense oligonucleotide; infection;
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
 KW immune system down-regulation; anti-inflammatory therapy; RT-PCR;
 KW primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9828442-A1.
 XX
 PD 02-JUL-1998.
 XX
 PF 19-DEC-1997; 97WO-US23619.
 XX
 PR 20-DEC-1996; 96US-0770565.
 PR 20-DEC-1996; 96US-0770564.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
 XX
 DR WPI; 1998-377670/32.
 XX
 PT New polynucleotide(s) anti:sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 65; Page 75; 80pp; English.
 XX
 CC This primer is used for the RT-PCR amplification of an RNA component of
 CC human telomerase (hTR). This is used in the method of invention of
 CC determining the amount of hTR in a sample. The method comprises
 CC amplifying a sequence of hTR and a control polynucleotide from a sample
 CC and determining an amount of amplified hTR and an amount of amplified
 CC control polynucleotide. The amount of amplified hTR is normalised with
 CC respect to the amount of amplified control polynucleotide to provide a
 CC normalised amount of hTR which provides a determination of the amount of
 CC hTR in the sample. The invention provides antisense oligonucleotides to
 CC the hTR which may specifically be used for detection of an RNA component
 CC of human telomerase in a sample. This is useful for diagnosing cancer
 CC (especially neuroblastoma, bladder, colon and prostate cancer), and
 CC providing prognosis for a cancer patient. The antisense oligonucleotides
 CC can be used for inhibiting telomerase activity in both cultured cells and
 CC in cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in anti-
 CC inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX
 SQ Sequence 27 BP; 7 A; 3 C; 10 G; 7 T; 0 other;
 XX
 Query Match 100.0%; Score 19; DB 19; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATGAACGGTGG 19
 |||||
 Db 5 GCTCTAGATGAACGGTGG 23
 |||||

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 Job time : 126.571 secs

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- 37: em_htg_vrt.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AR063833	AR063833 Sequence
2	19	100.0	26	6	A94988	A94988 Sequence 2
3	19	100.0	26	6	AR016055	AR016055 Sequence
4	19	100.0	26	6	AR028786	AR028786 Sequence
5	19	100.0	26	6	AR059216	AR059216 Sequence
6	19	100.0	26	6	AR075527	AR075527 Sequence
7	19	100.0	26	6	AR161925	AR161925 Sequence
8	19	100.0	26	6	AX022187	AX022187 Sequence
9	19	100.0	26	6	AX033377	AX033377 Sequence
10	19	100.0	26	6	AX468455	AX468455 Sequence
11	19	100.0	26	6	BD011297	BD011297 Human tel
12	19	100.0	26	6	E36508	E36508 Method for
13	19	100.0	26	6	E37046	E37046 Human telom
14	19	100.0	26	6	I31770	I31770 Sequence 23
15	19	100.0	27	6	AR063850	AR063850 Sequence
16	19	100.0	27	6	AX317989	AX317989 Sequence
17	19	100.0	30	6	AR063832	AR063832 Sequence
18	19	100.0	30	6	AX465471	AX465471 Sequence
19	18	94.7	30	6	A84596	A84596 Sequence 6
20	18	94.7	30	6	AR079893	AR079893 Sequence
21	15	78.9	15	6	AR063834	AR063834 Sequence
22	13	68.4	18	6	BD011244	BD011244 Human tel
23	13	68.4	18	6	E36993	E36993 Human telom
24	13	68.4	28	6	AX298137	AX298137 Sequence
25	12	63.2	17	6	AX099957	AX099957 Sequence
26	12	63.2	25	6	I04124	I04124 Sequence 8
27	12	63.2	26	6	AR000025	AR000025 Sequence
28	12	63.2	26	6	AR169136	AR169136 Sequence
29	12	63.2	26	6	AR202623	AR202623 Sequence
30	12	63.2	26	6	AX036237	AX036237 Sequence
31	12	63.2	30	6	I25474	I25474 Sequence 3
32	12	63.2	36	6	I04342	I04342 Sequence 6
33	12	63.2	39	6	E49124	E49124 Novel G pro
34	12	63.2	39	6	E50834	E50834 Novel G pro
35	11	57.9	11	6	AR063835	AR063835 Sequence
36	11	57.9	19	6	AX244257	AX244257 Sequence
37	11	57.9	21	6	AR193717	AR193717 Sequence
38	11	57.9	22	6	AR205029	AR205029 Sequence
39	11	57.9	22	6	AX082540	AX082540 Sequence
40	11	57.9	22	6	AX370655	AX370655 Sequence
41	11	57.9	23	6	AR112025	AR112025 Sequence
42	11	57.9	24	6	A91468	A91468 Sequence 10
43	11	57.9	24	6	AX085592	AX085592 Sequence
44	11	57.9	24	6	AX196969	AX196969 Sequence
45	11	57.9	26	6	AR179447	AR179447 Sequence

ALIGNMENTS

RESULT 1
AR063833
LOCUS
DEFINITION
Sequence 9 from patent US 5846723.
ACCESSION
AR063833
VERSION
AR063833.1 GI:5993141
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE
Methods for detecting the RNA component of telomerase
JOURNAL
Patent: US 5846723-A 9 08-DEC-1998;
FEATURES
Location/Qualifiers

AR063833
Sequence 9 from patent US 5846723.
AR063833.1 GI:5993141
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 19)
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 9 08-DEC-1998;
Location/Qualifiers

linear DNA 19 bp PAT 29-SRP-1999

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source 1. .19
BASE COUNT 5 a 3 c 7 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 1 GCTCTAGAAATGAACGGTGG 19

RESULT 2
A94988
LOCUS A94988 26 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 2 from Patent EP0926245.
ACCESSION A94988
VERSION A94988.1 GI:6779168
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Method for detection of carcinoma of the urinary bladder within a
urine sample
JOURNAL Patent: EP 0926245-A 2 30-JUN-1999;
FEATURES Roche Diagnostics GmbH (DE)
source Location/Qualifiers
1. .26
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 3
AR016055
LOCUS AR016055 26 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 23 from patent US 5776679.
ACCESSION AR016055
VERSION AR016055.1 GI:3972332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
FEATURES Location/Qualifiers
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/organism="unknown"
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 4
AR028786
LOCUS AR028786 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5858777.
ACCESSION AR028786
VERSION AR028786.1 GI:5940759
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLE Methods and reagents for regulating telomere length and telomerase
activity
JOURNAL Patent: US 5858777-A 26 12-JAN-1999;
FEATURES Location/Qualifiers
source 1. .26
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BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 5
AR059216
LOCUS AR059216 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5837857.
ACCESSION AR059216
VERSION AR059216.1 GI:5984793
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 23 17-NOV-1998;
FEATURES Location/Qualifiers
source 1. .26
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BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 6
AR075527
LOCUS AR075527 26 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5958680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
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TITLE Mammalian telomerase
JOURNAL Patent: US 595860-A 24 28-SEP-1999;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 7
LOCUS AR161925 26 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 23 from patent US 6258535.
ACCESSION AR161925
VERSION AR161925.1 GI:16228953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 23 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 8
LOCUS AX022187 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent EP0953042.
ACCESSION AX022187
VERSION AX022187.1 GI:10045855
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Andrews,W.H., Villeponteau,B., Adams,R.R. and Peng,J.
TITLE Methods and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: EP 0953042-A 26 03-NOV-1999;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 9
LOCUS AX033377 26 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 9 from Patent WO0046601.
ACCESSION AX033377
VERSION AX033377.1 GI:10280151
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Larsen,P. and Skaaneeng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 9 10-AUG-2000;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 10
LOCUS AX468455 26 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 5 from Patent WO0218652.
ACCESSION AX468455
VERSION AX468455.1 GI:21901291
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kopreski,M.S. and Gocke,C.D.
TITLE Method for detection of htr and htert telomerase-associated rna in plasma or serum
JOURNAL Patent: WO 0218652-A 5 07-MAR-2002;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 3 c 9 g 7 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 11
LOCUS BD011297 26 bp DNA linear PAT 31-JAN-2002

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DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011297
VERSION BD011297.1 GI:18639670
KEYWORDS JP 2001081042-A/254.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
        Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 254 27-MAR-2001;
        GERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 2001081042-A/254
        PD 27-MAR-2001
        PF 27-JUL-2000 JP 2000227474
        PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
        25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
        09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
        14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
        R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
        MORIN,
        PI CALVIN B HARLEY,WILLIAM H ANDREWS
        PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
        PC C07K5/10,
        PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
        C12N15/09,C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
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        BASE COUNT 7 a 3 c 9 g 7 t
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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 12
E36508
LOCUS Human telomerase catalytic subunit
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36508
VERSION E36508.1 GI:13022705
KEYWORDS JP 1999243995-A/2.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Thomas,E.
TITLE Method for detecting bladder cancer in urine samples
JOURNAL Patent: JP 1999243995-A 2 14-SEP-1999;
        ROCHE DIAGNOSTICS GMBH
COMMENT OS Artificial Sequence
        PN JP 1999243995-A/2
        PD 14-SEP-1999
        PF 22-DEC-1998 JP 1998365689
        PR 22-DEC-1997 DE 19757300.2
        PI THOMAS ENRIHI

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PC C12Q1/68//C12N1/00
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19
Db 5 GCTCTAGATGAACGGTGG 23

RESULT 13
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LOCUS Human telomerase catalytic subunit promoter.
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E37046
VERSION E37046.1 GI:13023009
KEYWORDS JP 1999253177-A/254.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
        Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 254 21-SEP-1999;
        JERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 1999253177-A/254
        PD 21-SEP-1999
        PF 15-OCT-1998 JP 1998320169
        PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419, PR
        25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843, PR
        09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312, PR
        14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
        R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
        MORIN,
        PI CALVIN B HARLEY,WILLIAM H ANDREWS
        PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
        PC C12Q1/02,
        PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
        C07K16/40,
        PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
        C12R1:84),
        PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
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        CC Topology: Linear;
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BASE COUNT 7 a 3 c 9 g 7 t
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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGG 19

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Db          5 GCTCTAGAAATGAACGGTGG 23
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LOCUS
DEFINITION  Sequence 23 from patent US 5583016.
ACCESSION  I31770
VERSION    I31770.1 GI:1822561
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE     Mammalian telomerase
JOURNAL   Patent: US 5583016-A 23 10-DEC-1996;
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BASE COUNT 7 a      3 c      9 g      7 t
ORIGIN

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QY 1 GCTCTAGAAATGAACGGTGG 19
|||||
Db 5 GCTCTAGAAATGAACGGTGG 23

RESULT 15
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LOCUS
DEFINITION  Sequence 26 from patent US 5846723.
ACCESSION  AR063850
VERSION    AR063850.1 GI:5993158
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 27)
AUTHORS   Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE     Methods for detecting the RNA component of telomerase
JOURNAL   Patent: US 5846723-A 26 08-DEC-1998;
FEATURES
source    1..27
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BASE COUNT 7 a      3 c     10 g      7 t
ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACGGTGG 19
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Db 5 GCTCTAGAAATGAACGGTGG 23

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Job time : 221.422 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15	100.0	21	1	PCT-US03-04088-543 Sequence 543, App
C 3	15	100.0	21	1	PCT-US03-04088-547 Sequence 547, App
C 4	15	100.0	21	1	PCT-US03-04088-551 Sequence 551, App
C 5	15	100.0	21	1	PCT-US03-04088-555 Sequence 555, App
C 6	15	100.0	21	1	PCT-US03-04088-559 Sequence 559, App
C 7	15	100.0	23	1	PCT-US03-04088-520 Sequence 520, App
C 8	15	100.0	23	1	PCT-US03-04088-521 Sequence 521, App
C 9	15	100.0	26	6	US-09-721-456-598 Sequence 598, App
C 10	15	100.0	26	9	US-10-325-810-598 Sequence 598, App
C 11	15	100.0	26	9	US-10-325-810-598 Sequence 598, App
C 12	15	100.0	26	9	US-10-359-935-23 Sequence 23, Appl
C 13	15	100.0	30	10	US-10-330-872-5 Sequence 5, Appl
C 14	15	100.0	30	10	US-10-330-872A-5 Sequence 5, Appl
C 15	14	93.3	23	9	US-10-310-188-36216 Sequence 36216, A
C 16	14	93.3	25	12	US-60-427-808-952738 Sequence 952738, A
C 17	14	93.3	25	13	US-60-469-545-13722 Sequence 13722, A
C 18	13.4	89.3	18	6	US-09-721-456-543 Sequence 543, App
C 19	13.4	89.3	18	9	US-10-325-810-543 Sequence 543, App
C 20	13.4	89.3	25	7	US-09-954-445A-54976 Sequence 54976, A

C 21	13.4	89.3	25	9	US-10-355-577-981444 Sequence 981444, App
C 22	13.4	89.3	25	12	US-60-427-836-494214 Sequence 494214, App
C 23	13	86.7	21	1	PCT-US03-04088-538 Sequence 538, App
C 24	13	86.7	21	1	PCT-US03-04088-542 Sequence 542, App
C 25	13	86.7	21	1	PCT-US03-04088-546 Sequence 546, App
C 26	13	86.7	21	1	PCT-US03-04088-550 Sequence 550, App
C 27	13	86.7	21	1	PCT-US03-04088-554 Sequence 554, App
C 28	13	86.7	21	1	PCT-US03-04088-558 Sequence 558, App
C 29	13	86.7	25	6	US-09-660-222-3845 Sequence 3845, App
C 30	13	86.7	25	6	US-09-660-222-3846 Sequence 3846, App
C 31	13	86.7	25	6	US-09-660-222-3854 Sequence 3854, App
C 32	13	86.7	25	9	US-10-098-263B-118949 Sequence 118949, App
C 33	13	86.7	25	9	US-10-355-577-173196 Sequence 173196, App
C 34	13	86.7	25	12	US-60-427-808-738286 Sequence 738286, App
C 35	13	86.7	25	12	US-60-427-836-267834 Sequence 267834, App
C 36	12.4	82.7	25	6	US-09-660-222-121265 Sequence 121265, App
C 37	12.4	82.7	25	9	US-10-355-577-70333 Sequence 70333, A
C 38	12.4	82.7	25	9	US-10-355-577-482963 Sequence 482963, App
C 39	12.4	82.7	25	9	US-10-355-577-704066 Sequence 704066, App
C 40	12.4	82.7	25	9	US-10-355-577-751232 Sequence 751232, App
C 41	12.4	82.7	25	9	US-10-355-577-956874 Sequence 956874, App
C 42	12.4	82.7	25	12	US-60-427-808-51166 Sequence 51166, A
C 43	12.4	82.7	25	12	US-60-427-808-44453 Sequence 44453, App
C 44	12.4	82.7	25	12	US-60-427-808-952737 Sequence 952737, App
C 45	12.4	82.7	25	12	US-60-427-836-153966 Sequence 153966, App

ALIGNMENTS

RESULT 1
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggan, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
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; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)-(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0%; Score 15; DB 1; Length 21;


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; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 21
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; ORGANISM: Artificial
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; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
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; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
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; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; PCT-US03-04088-551

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. NO. 1.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 1 GCUCUAGAAGAACG 15

RESULT 5
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 555
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
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; FEATURE:
; NAME/KEY: misc_feature
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; FEATURE:
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; FEATURE:
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; LOCATION: (19)..(19)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:

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NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-555

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
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Db 19 GCTCTAGAAATGAACG 5

RESULT 6

PCT-US03-04088-559
; Sequence 559, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
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; LOCATION: (2)..(5)
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; OTHER INFORMATION: 2'-deoxy-2'-fluoro
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; NAME/KEY: misc_feature
; LOCATION: (11)..(13)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
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; LOCATION: (15)..(16)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
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; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-559

Query Match 100.0%; Score 15; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
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Db 1 GCUCUAGAAUGAACG 15

RESULT 7

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; Sequence 520, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 520
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-520

Query Match 100.0%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 23 GCTCTAGAAATGAACG 9

RESULT 8
 PCT-US03-04088-521/c
 ; Sequence 521, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 521
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
 ; OTHER INFORMATION: region
 ; OTHER INFORMATION: region
 PCT-US03-04088-521

Query Match 100.0%; Score 15; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 21 GCTCTAGAAATGAACG 7

RESULT 9
 US-09-721-456-598
 ; Sequence 598, Application US/09721456
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco

STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 598:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..26
 OTHER INFORMATION: /note= "R3c primer"
 SEQUENCE DESCRIPTION: SEQ ID NO: 598:
 US-09-721-456-598

Query Match 100.0%; Score 15; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
 Db 5 GCTCTAGAAATGAACG 19

RESULT 10
 US-10-325-810-598
 ; Sequence 598, Application US/10325810
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.

Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note= "R3c primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 598

US-10-325-810-598
Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 11

US-10-359-935-23
Sequence 23, Application US/10359935
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
Feng, Junli
Funk, Walter
Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-359-935-23

Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACG 15
Db 5 GCTCTAGATGAACG 19

RESULT 12
US-10-330-872-5
Sequence 5, Application US/10330872
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Weinrich, Scott
APPLICANT: Atkinson III, Edward
APPLICANT: Lichtsteiner, Serge
APPLICANT: Vasserot, Alain
APPLICANT: Pruzan, Ronald
TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: 011/006C